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From: Slobodyansky, Elizabeth
Sent: Wednesday, April 07, 2004 5:41 PM
To: STIC-Biotech/ChemLib
Subject: 10/076,604

Please search for case 10/076,604:

SEQ ID NO: 208 against commercial databases.

Thank you.

Elizabeth Slobodyansky, PhD

Primary Examiner

Art Unit 1652
REM 3A65
571-272-0941
MAILBOX 3C70

Searcher:_____
Phone:_____
Location:_____
Date Picked Up: 4/8/04
Date Completed: 4/8/04
Searcher Prep/Review:_____
Clerical:_____
Online time:_____

TYPE OF SEARCH:
NA Sequences:_____
AA Sequences: 1
Structures:_____
Bibliographic:_____
Litigation:_____
Full text:_____
Patent Family:_____
Other:_____

VENDOR/COST (where applic.)
STN:_____
DIALOG:_____
Questel/Orbit:_____
DRLink:_____
Lexis/Nexis:_____
Sequence Sys.: 0.05 P
WWW/Internet:_____
Other (specify):_____

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: April 8, 2004, 09:27:16 ; Search time 55 Seconds
(without alignments)
313.371 Million cell updates/sec

Title: US-10-076-604-208
Perfect score: 351
Sequence: 1 EVVREVCSEQAETGPCRAAI.....GNRNNFDTEEYCMAVCGSAI 61

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_29Jan04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	351	100.0	61	3	AAY68159	Aay68159 Kunitz pr
2	351	100.0	61	3	AAY68056	Aay68056 Kunitz pr
3	351	100.0	146	3	AAY68055	Aay68055 Yeast mat
4	347	98.9	61	3	AAY68169	Aay68169 Kunitz pr
5	347	98.9	61	3	AAY68175	Aay68175 Kunitz pr
6	347	98.9	61	4	AAU09329	Aau09329 Human KPI
7	347	98.9	61	4	AAU09335	Aau09335 Human KPI
8	346	98.6	61	3	AAY68058	Aay68058 Kunitz pr
9	346	98.6	61	3	AAY68050	Aay68050 Kunitz pr
10	346	98.6	61	3	AAY68157	Aay68157 Kunitz pr
11	346	98.6	61	3	AAY68168	Aay68168 Kunitz pr
12	346	98.6	61	4	AAU09319	Aau09319 Human KPI
13	346	98.6	61	4	AAU09317	Aau09317 Human KPI
14	346	98.6	146	3	AAY68049	Aay68049 Yeast mat
15	346	98.6	146	3	AAY68057	Aay68057 Yeast mat
16	343	97.7	61	2	AAW18427	Aaw18427 KPI(-4 to
17	343	97.7	61	2	AAW18401	Aaw18401 KPI(-4 to
18	343	97.7	61	3	AAY68182	Aay68182 KPI-P48 p
19	343	97.7	61	3	AAY68124	Aay68124 Kunitz pr
20	343	97.7	61	3	AAY68036	Aay68036 Kunitz pr
21	343	97.7	61	3	AAY68162	Aay68162 Kunitz pr
22	343	97.7	61	4	AAU09322	Aau09322 Human KPI
23	343	97.7	61	4	AAU09216	Aau09216 Human KPI
24	343	97.7	146	2	AAW18448	Aaw18448 Alpha mat
25	343	97.7	146	3	AAY68027	Aay68027 Yeast mat
26	343	97.7	146	3	AAY68181	Aay68181 Yeast mat
27	343	97.7	146	4	AAU09207	Aau09207 Yeast alp
28	342	97.4	61	3	AAY68167	Aay68167 Kunitz pr
29	342	97.4	61	3	AAY68174	Aay68174 Kunitz pr
30	342	97.4	61	4	AAU09327	Aau09327 Human KPI
31	342	97.4	61	4	AAU09334	Aau09334 Human KPI
32	341	97.2	61	3	AAY68166	Aay68166 Kunitz pr
33	341	97.2	61	3	AAY68155	Aay68155 Kunitz pr
34	341	97.2	61	3	AAY68052	Aay68052 Kunitz pr
35	341	97.2	61	4	AAU09315	Aau09315 Human KPI
36	341	97.2	61	4	AAU09326	Aau09326 Human KPI
37	341	97.2	61	4	AAU09328	Aau09328 Human KPI
38	341	97.2	146	3	AAY68051	Aay68051 Yeast mat
39	340.5	97.0	62	2	AAW18433	Aaw18433 KPI(-4 to
40	340	96.9	61	3	AAY68170	Aay68170 Kunitz pr
41	340	96.9	61	4	AAU09330	Aau09330 Human KPI
42	339	96.6	61	2	AAW18404	Aaw18404 KPI(-4 to
43	339	96.6	61	2	AAW18430	Aaw18430 KPI(-4 to
44	339	96.6	61	2	AAW18426	Aaw18426 KPI(-4 to
45	339	96.6	61	3	AAY68122	Aay68122 Kunitz pr

ALIGNMENTS

RESULT 1
AAY68159
ID AAY68159 standard; protein; 61 AA.
XX
AC AAY68159;
XX
DT 13-APR-2000 (first entry)
XX
DE Kunitz protease inhibitor variant BG022.
XX
KW Kunitz protease inhibitor; KPI; serine protease; kallikrein; plasmin;
KW amyloid precursor protein; coagulation factor; blood loss; cardiant;
KW cardiopulmonary bypass surgery; anticoagulant; anti-inflammatory;
KW anti-arthritic; thrombolytic; antirheumatic; antipsoriatic;
KW immunosuppressant; pancreatitis; deep vein thrombosis; psoriasis;
KW rheumatoid arthritis; myocardial infarction; transplant rejection.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO9963090-A2.
XX
PD 09-DEC-1999.
XX
PF 03-JUN-1999; 99WO-US012276.
XX
PR 03-JUN-1998; 98US-0087885P.
XX
PA (SCIO-) SCIOS INC.
XX
PI White RT, Damm D, Lesikar DD, Mcfadden K, Garrick BL, Lucas AB;
PI Pollitt NS, Lam AO;
XX
DR WPI; 2000-105699/09.
XX
PT Novel enzyme inhibitors especially used to reduce postoperative bleeding.
XX
PS Example 4; Fig 64; 151pp; English.
XX
CC The present invention describes protease inhibitors that are analogues of
CC the Kunitz protease inhibitor (KPI) domain of the amyloid precursor
CC protein. The protease inhibitors can be used used to treat or prevent
CC disorders associated with increased activity of serine proteases,
CC specifically blood loss during surgery (particularly cardiopulmonary
CC bypass surgery where plasma proteases are activated by contact with
CC surfaces in the heart-lung machine), but also other conditions such as
CC pancreatitis; deep vein thrombosis; rheumatoid arthritis; psoriasis;
CC myocardial infarction; and transplant rejection. They are also for organ

```
CC   preservation and to promote wound healing. In vitro the protease
CC   inhibitors may be used to inhibit serine proteases during preparation of
CC   cell extracts. The protease inhibitors are based on a human peptide
CC   sequence so are unlikely to be immunogenic, can be produced at high
CC   levels in recombinant expression systems, and can inhibit a wide range of
CC   serine proteases. They are more potent or specific than known inhibitors.
CC   The present sequence represents a KPI variant which is given in an
CC   example from the present invention
XX
SQ   Sequence 61 AA;

  Query Match             100.0%;  Score 351;  DB 3;  Length 61;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-31;
  Matches   61;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 EVVREVCSEQAETGPCRAAIYHWYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMAVCGSA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 EVVREVCSEQAETGPCRAAIYHWYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMAVCGSA 60

Qy         61 I 61
              |
Db         61 I 61


RESULT 2
AAY68056
ID   AAY68056 standard; protein; 61 AA.
XX
AC   AAY68056;
XX
DT   13-APR-2000  (first entry)
XX
DE   Kunitz protease inhibitor analogue protein sequence Fig 40.
XX
KW   Kunitz protease inhibitor; KPI; serine protease; kallikrein; plasmin;
KW   amyloid precursor protein; coagulation factor; blood loss; cardiant;
KW   cardiopulmonary bypass surgery; anticoagulant; anti-inflammatory;
KW   anti-arthritic; thrombolytic; antirheumatic; antipsoriatic;
KW   immunosuppressant; pancreatitis; deep vein thrombosis; psoriasis;
KW   rheumatoid arthritis; myocardial infarction; transplant rejection.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO9963090-A2.
XX
PD   09-DEC-1999.
XX
PF   03-JUN-1999;   99WO-US012276.
XX
PR   03-JUN-1998;   98US-0087885P.
XX
PA   (SCIO-) SCIOS INC.
XX
PI   White RT,  Damm D,  Lesikar DD,  Mcfadden K,  Garrick BL,  Lucas AB;
PI   Pollitt NS,  Lam AO;
XX
DR   WPI; 2000-105699/09.
XX
PT   Novel enzyme inhibitors especially used to reduce postoperative bleeding.
XX
PS   Example 3; Fig 40; 151pp; English.
XX
CC   The present invention describes protease inhibitors that are analogues of
CC   the Kunitz protease inhibitor (KPI) domain of the amyloid precursor
CC   protein. The protease inhibitors can be used used to treat or prevent
CC   disorders associated with increased activity of serine proteases,
CC   specifically blood loss during surgery (particularly cardiopulmonary
CC   bypass surgery where plasma proteases are activated by contact with
CC   surfaces in the heart-lung machine), but also other conditions such as
CC   pancreatitis; deep vein thrombosis; rheumatoid arthritis; psoriasis;
CC   myocardial infarction; and transplant rejection. They are also for organ
CC   preservation and to promote wound healing. In vitro the protease
CC   inhibitors may be used to inhibit serine proteases during preparation of
CC   cell extracts. The protease inhibitors are based on a human peptide
CC   sequence so are unlikely to be immunogenic, can be produced at high
CC   levels in recombinant expression systems, and can inhibit a wide range of
CC   serine proteases. They are more potent or specific than known inhibitors.
CC   The present sequence is given in an example from the present invention
XX
SQ   Sequence 61 AA;

  Query Match             100.0%;  Score 351;  DB 3;  Length 61;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-31;
  Matches   61;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 EVVREVCSEQAETGPCRAAIYHWYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMAVCGSA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 EVVREVCSEQAETGPCRAAIYHWYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMAVCGSA 60

Qy         61 I 61
              |
Db         61 I 61


RESULT 3
AAY68055
ID   AAY68055 standard; protein; 146 AA.
XX
AC   AAY68055;
XX
DT   13-APR-2000  (first entry)
XX
DE   Yeast mating-factor-KPI(-4-57) fusion protein sequence Fig 23.
XX
KW   Kunitz protease inhibitor; KPI; serine protease; kallikrein; plasmin;
KW   amyloid precursor protein; coagulation factor; blood loss; cardiant;
KW   cardiopulmonary bypass surgery; anticoagulant; anti-inflammatory;
KW   anti-arthritic; thrombolytic; antirheumatic; antipsoriatic;
KW   immunosuppressant; pancreatitis; deep vein thrombosis; psoriasis;
KW   rheumatoid arthritis; myocardial infarction; transplant rejection.
XX
OS   Homo sapiens.
OS   Saccharomyces cerevisiae.
OS   Synthetic.
XX
PN   WO9963090-A2.
XX
PD   09-DEC-1999.
XX
PF   03-JUN-1999;   99WO-US012276.
XX
PR   03-JUN-1998;   98US-0087885P.
XX
PA   (SCIO-) SCIOS INC.
XX
PI   White RT,  Damm D,  Lesikar DD,  Mcfadden K,  Garrick BL,  Lucas AB;
PI   Pollitt NS,  Lam AO;
XX
DR   WPI; 2000-105699/09.
DR   N-PSDB; AAZ57538.
XX
PT   Novel enzyme inhibitors especially used to reduce postoperative bleeding.
XX
PS   Example 3; Fig 23; 151pp; English.
XX
CC   The present invention describes protease inhibitors that are analogues of
CC   the Kunitz protease inhibitor (KPI) domain of the amyloid precursor
CC   protein. The protease inhibitors can be used used to treat or prevent
CC   disorders associated with increased activity of serine proteases,
CC   specifically blood loss during surgery (particularly cardiopulmonary
CC   bypass surgery where plasma proteases are activated by contact with
CC   surfaces in the heart-lung machine), but also other conditions such as
CC   pancreatitis; deep vein thrombosis; rheumatoid arthritis; psoriasis;
CC   myocardial infarction; and transplant rejection. They are also for organ
CC   preservation and to promote wound healing. In vitro the protease
```

CC inhibitors may be used to inhibit serine proteases during preparation of
CC cell extracts. The protease inhibitors are based on a human peptide
CC sequence so are unlikely to be immunogenic, can be produced at high
CC levels in recombinant expression systems, and can inhibit a wide range of
CC serine proteases. They are more potent or specific than known inhibitors.
CC The present sequence is given in an example from the present invention
XX
SQ Sequence 146 AA;

Query Match 100.0%; Score 351; DB 3; Length 146;
Best Local Similarity 100.0%; Pred. No. 2.6e-31;
Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVVREVCSEQAETGPCRAAIYHWYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMAVCGSA 60
Db 86 EVVREVCSEQAETGPCRAAIYHWYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMAVCGSA 145

Qy 61 I 61
Db 146 I 146

RESULT 4
AAY68169
ID AAY68169 standard; protein; 61 AA.
XX
AC AAY68169;
XX
DT 13-APR-2000 (first entry)
XX
DE Kunitz protease inhibitor variant BG034.
XX
KW Kunitz protease inhibitor; KPI; serine protease; kallikrein; plasmin;
KW amyloid precursor protein; coagulation factor; blood loss; cardiant;
KW cardiopulmonary bypass surgery; anticoagulant; anti-inflammatory;
KW anti-arthritic; thrombolytic; antirheumatic; antipsoriatic;
KW immunosuppressant; pancreatitis; deep vein thrombosis; psoriasis;
KW rheumatoid arthritis; myocardial infarction; transplant rejection.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO9963090-A2.
XX
PD 09-DEC-1999.
XX
PF 03-JUN-1999; 99WO-US012276.
XX
PR 03-JUN-1998; 98US-0087885P.
XX
PA (SCIO-) SCIOS INC.
XX
PI White RT, Damm D, Lesikar DD, Mcfadden K, Garrick BL, Lucas AB;
PI Pollitt NS, Lam AO;
XX
DR WPI; 2000-105699/09.
XX
PT Novel enzyme inhibitors especially used to reduce postoperative bleeding.
XX
PS Example 4; Fig 64; 151pp; English.
XX
CC The present invention describes protease inhibitors that are analogues of
CC the Kunitz protease inhibitor (KPI) domain of the amyloid precursor
CC protein. The protease inhibitors can be used used to treat or prevent
CC disorders associated with increased activity of serine proteases,
CC specifically blood loss during surgery (particularly cardiopulmonary
CC bypass surgery where plasma proteases are activated by contact with
CC surfaces in the heart-lung machine), but also other conditions such as
CC pancreatitis; deep vein thrombosis; rheumatoid arthritis; psoriasis;
CC myocardial infarction; and transplant rejection. They are also for organ
CC preservation and to promote wound healing. In vitro the protease
CC inhibitors may be used to inhibit serine proteases during preparation of
CC cell extracts. The protease inhibitors are based on a human peptide
CC sequence so are unlikely to be immunogenic, can be produced at high
CC levels in recombinant expression systems, and can inhibit a wide range of
CC serine proteases. They are more potent or specific than known inhibitors.
CC The present sequence represents a KPI variant which is given in an
CC example from the present invention
XX
SQ Sequence 61 AA;

Query Match 98.9%; Score 347; DB 3; Length 61;
Best Local Similarity 98.4%; Pred. No. 3e-31;
Matches 60; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVVREVCSEQAETGPCRAAIYHWYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMAVCGSA 60
Db 1 EVVREVCSEQAESGPCRAAIYHWYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMAVCGSA 60

Qy 61 I 61
Db 61 I 61

RESULT 5
AAY68175
ID AAY68175 standard; protein; 61 AA.
XX
AC AAY68175;
XX
DT 13-APR-2000 (first entry)
XX
DE Kunitz protease inhibitor variant BG026.
XX
KW Kunitz protease inhibitor; KPI; serine protease; kallikrein; plasmin;
KW amyloid precursor protein; coagulation factor; blood loss; cardiant;
KW cardiopulmonary bypass surgery; anticoagulant; anti-inflammatory;
KW anti-arthritic; thrombolytic; antirheumatic; antipsoriatic;
KW immunosuppressant; pancreatitis; deep vein thrombosis; psoriasis;
KW rheumatoid arthritis; myocardial infarction; transplant rejection.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO9963090-A2.
XX
PD 09-DEC-1999.
XX
PF 03-JUN-1999; 99WO-US012276.
XX
PR 03-JUN-1998; 98US-0087885P.
XX
PA (SCIO-) SCIOS INC.
XX
PI White RT, Damm D, Lesikar DD, Mcfadden K, Garrick BL, Lucas AB;
PI Pollitt NS, Lam AO;
XX
DR WPI; 2000-105699/09.
XX
PT Novel enzyme inhibitors especially used to reduce postoperative bleeding.
XX
PS Example 4; Fig 64; 151pp; English.
XX
CC The present invention describes protease inhibitors that are analogues of
CC the Kunitz protease inhibitor (KPI) domain of the amyloid precursor
CC protein. The protease inhibitors can be used used to treat or prevent
CC disorders associated with increased activity of serine proteases,
CC specifically blood loss during surgery (particularly cardiopulmonary
CC bypass surgery where plasma proteases are activated by contact with
CC surfaces in the heart-lung machine), but also other conditions such as
CC pancreatitis; deep vein thrombosis; rheumatoid arthritis; psoriasis;
CC myocardial infarction; and transplant rejection. They are also for organ
CC preservation and to promote wound healing. In vitro the protease
CC inhibitors may be used to inhibit serine proteases during preparation of
CC cell extracts. The protease inhibitors are based on a human peptide
CC sequence so are unlikely to be immunogenic, can be produced at high

```
CC   levels in recombinant expression systems, and can inhibit a wide range of
CC   serine proteases. They are more potent or specific than known inhibitors.
CC   The present sequence represents a KPI variant which is given in an
CC   example from the present invention
XX
SQ   Sequence 61 AA;

  Query Match             98.9%;  Score 347;  DB 3;  Length 61;
  Best Local Similarity   98.4%;  Pred. No. 3e-31;
  Matches   60;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 EVVREVCSEQAETGPCRAAIYHWYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMAVCGSA 60
              |||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db          1 EVVREVCSEQAETGPCRGAIYHWYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMAVCGSA 60

Qy         61 I 61
              |
Db         61 I 61


RESULT 6
AAU09329
ID   AAU09329 standard; protein; 61 AA.
XX
AC   AAU09329;
XX
DT   03-JAN-2002  (first entry)
XX
DE   Human KPI variant, BG034.
XX
KW   Human; serine protease inhibitor; Kunitz Protease Inhibitor; KPI;
KW   amyloid precursor protein; kallikrein; plasmin; coagulation factor;
KW   blood loss; surgery; respiratory disorder; deep vein thrombosis;
KW   inflammatory bowel disease; cardiovascular disorder; haemostatic; mutant;
KW   mutein; variant.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   US2001020003-A1.
XX
PD   06-SEP-2001.
XX
PF   21-JAN-1999;   99US-00234874.
XX
PR   21-JAN-1999;   99US-00234874.
XX
PA   (WHIT/) WHITE R T.
PA   (DAMM/) DAMM D.
PA   (LESI/) LESIKAR D D.
PA   (MCFA/) MCFADDEN K.
PA   (GARR/) GARRICK B L.
XX
PI   White RT,  Damm D,  Lesikar DD,  Mcfadden K,  Garrick BL;
XX
DR   WPI; 2001-570185/64.
XX
PT   New serine protease inhibitors useful in ameliorating, treating or
PT   preventing clinical conditions associated with increased activity of
PT   serine proteases e.g. pulmonary injury, pacreatitis, deep vein
PT   thrombosis, wound healing.
XX
PS   Example 4; Fig 46; 74pp; English.
XX
CC   The present invention relates to serine protease inhibitor peptides.
CC   These peptides which are analogues of the Kunitz Protease Inhibitor (KPI)
CC   domain of amyloid precursor protein bind and inhibit the activity of
CC   serine proteases such as kallikrein, plasmin, and coagulation factors
CC   (e.g. factors VIIa, IXa, Xa, XIa, and XIIa). The protease inhibitors of
CC   the invention are useful for treating blood loss during surgery. The
CC   protease inhibitors may also be used in ameliorating, treating or
CC   preventing clinical conditions associated with increased activity of
CC   serine proteases, in reducing tissue damage caused by activation of the
CC   proteases of the contact pathway of the blood during surgical procedures
CC   such as cardiopulmonary bypass, or reducing serine protease-associated
CC   peri-operative and post-operative blood loss. Examples of other clinical
CC   conditions associated with increased serine protease activity for which
CC   the peptides may be used as treatment includes pulmonary injury,
CC   pancreatitis, allergy-induced protease release, deep vein thrombosis,
CC   thrombocytopaenia, rheumatoid arthritis, adult respiratory distress
CC   syndrome, chronic inflammatory bowel disease, psoriasis,
CC   hyperfibrinolytic haemorrhage, organ preservation, wound healing and
CC   myocardial infarction. AAU09229-AAU09339 represent human KPI variants of
CC   the present invention
XX
SQ   Sequence 61 AA;

  Query Match             98.9%;  Score 347;  DB 4;  Length 61;
  Best Local Similarity   98.4%;  Pred. No. 3e-31;
  Matches   60;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 EVVREVCSEQAETGPCRAAIYHWYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMAVCGSA 60
              |||||||||||||:|||||||||||||||||||||||||||||||||||||||||||||||
Db          1 EVVREVCSEQAESGPCRAAIYHWYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMAVCGSA 60

Qy         61 I 61
              |
Db         61 I 61


RESULT 7
AAU09335
ID   AAU09335 standard; protein; 61 AA.
XX
AC   AAU09335;
XX
DT   03-JAN-2002  (first entry)
XX
DE   Human KPI variant, BG026.
XX
KW   Human; serine protease inhibitor; Kunitz Protease Inhibitor; KPI;
KW   amyloid precursor protein; kallikrein; plasmin; coagulation factor;
KW   blood loss; surgery; respiratory disorder; deep vein thrombosis;
KW   inflammatory bowel disease; cardiovascular disorder; haemostatic; mutant;
KW   mutein; variant.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   US2001020003-A1.
XX
PD   06-SEP-2001.
XX
PF   21-JAN-1999;   99US-00234874.
XX
PR   21-JAN-1999;   99US-00234874.
XX
PA   (WHIT/) WHITE R T.
PA   (DAMM/) DAMM D.
PA   (LESI/) LESIKAR D D.
PA   (MCFA/) MCFADDEN K.
PA   (GARR/) GARRICK B L.
XX
PI   White RT,  Damm D,  Lesikar DD,  Mcfadden K,  Garrick BL;
XX
DR   WPI; 2001-570185/64.
XX
PT   New serine protease inhibitors useful in ameliorating, treating or
PT   preventing clinical conditions associated with increased activity of
PT   serine proteases e.g. pulmonary injury, pacreatitis, deep vein
PT   thrombosis, wound healing.
XX
PS   Example 4; Fig 46; 74pp; English.
XX
CC   The present invention relates to serine protease inhibitor peptides.
CC   These peptides which are analogues of the Kunitz Protease Inhibitor (KPI)
```

CC domain of amyloid precursor protein bind and inhibit the activity of
CC serine proteases such as kallikrein, plasmin, and coagulation factors
CC (e.g. factors VIIa, IXa, Xa, XIa, and XIIa). The protease inhibitors of
CC the invention are useful for treating blood loss during surgery. The
CC protease inhibitors may also be used in ameliorating, treating or
CC preventing clinical conditions associated with increased activity of
CC serine proteases, in reducing tissue damage caused by activation of the
CC proteases of the contact pathway of the blood during surgical procedures
CC such as cardiopulmonary bypass, or reducing serine protease-associated
CC peri-operative and post-operative blood loss. Examples of other clinical
CC conditions associated with increased serine protease activity for which
CC the peptides may be used as treatment includes pulmonary injury,
CC pancreatitis, allergy-induced protease release, deep vein thrombosis,
CC thrombocytopaenia, rheumatoid arthritis, adult respiratory distress
CC syndrome, chronic inflammatory bowel disease, psoriasis,
CC hyperfibrinolytic haemorrhage, organ preservation, wound healing and
CC myocardial infarction. AAU09229-AAU09339 represent human KPI variants of
CC the present invention
XX
SQ Sequence 61 AA;

Query Match 98.9%; Score 347; DB 4; Length 61;
Best Local Similarity 98.4%; Pred. No. 3e-31;
Matches 60; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy          1 EVVREVCSEQAETGPCRAAIYHWYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMAVCGSA 60
              ||||||||||||||||| |||||||||||||||||||||||||||||||||||||||||||
Db          1 EVVREVCSEQAETGPCRGAIYHWYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMAVCGSA 60

Qy         61 I 61
              |
Db         61 I 61
```

RESULT 8
AAY68058
ID AAY68058 standard; protein; 61 AA.
XX
AC AAY68058;
XX
DT 13-APR-2000 (first entry)
XX
DE Kunitz protease inhibitor analogue protein sequence Fig 41.
XX
KW Kunitz protease inhibitor; KPI; serine protease; kallikrein; plasmin;
KW amyloid precursor protein; coagulation factor; blood loss; cardiant;
KW cardiopulmonary bypass surgery; anticoagulant; anti-inflammatory;
KW anti-arthritic; thrombolytic; antirheumatic; antipsoriatic;
KW immunosuppressant; pancreatitis; deep vein thrombosis; psoriasis;
KW rheumatoid arthritis; myocardial infarction; transplant rejection.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO9963090-A2.
XX
PD 09-DEC-1999.
XX
PF 03-JUN-1999; 99WO-US012276.
XX
PR 03-JUN-1998; 98US-0087885P.
XX
PA (SCIO-) SCIOS INC.
XX
PI White RT, Damm D, Lesikar DD, Mcfadden K, Garrick BL, Lucas AB;
PI Pollitt NS, Lam AO;
XX
DR WPI; 2000-105699/09.
XX
PT Novel enzyme inhibitors especially used to reduce postoperative bleeding.
XX
PS Example 3; Fig 41; 151pp; English.
XX
CC The present invention describes protease inhibitors that are analogues of
CC the Kunitz protease inhibitor (KPI) domain of the amyloid precursor
CC protein. The protease inhibitors can be used used to treat or prevent
CC disorders associated with increased activity of serine proteases,
CC specifically blood loss during surgery (particularly cardiopulmonary
CC bypass surgery where plasma proteases are activated by contact with
CC surfaces in the heart-lung machine), but also other conditions such as
CC pancreatitis; deep vein thrombosis; rheumatoid arthritis; psoriasis;
CC myocardial infarction; and transplant rejection. They are also for organ
CC preservation and to promote wound healing. In vitro the protease
CC inhibitors may be used to inhibit serine proteases during preparation of
CC cell extracts. The protease inhibitors are based on a human peptide
CC sequence so are unlikely to be immunogenic, can be produced at high
CC levels in recombinant expression systems, and can inhibit a wide range of
CC serine proteases. They are more potent or specific than known inhibitors.
CC The present sequence is given in an example from the present invention
XX
SQ Sequence 61 AA;

Query Match 98.6%; Score 346; DB 3; Length 61;
Best Local Similarity 98.4%; Pred. No. 3.9e-31;
Matches 60; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy          1 EVVREVCSEQAETGPCRAAIYHWYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMAVCGSA 60
              ||||||||||| |||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 EVVREVCSEQAEVGPCRAAIYHWYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMAVCGSA 60

Qy         61 I 61
              |
Db         61 I 61
```

RESULT 9
AAY68050
ID AAY68050 standard; protein; 61 AA.
XX
AC AAY68050;
XX
DT 13-APR-2000 (first entry)
XX
DE Kunitz protease inhibitor analogue protein sequence Fig 37.
XX
KW Kunitz protease inhibitor; KPI; serine protease; kallikrein; plasmin;
KW amyloid precursor protein; coagulation factor; blood loss; cardiant;
KW cardiopulmonary bypass surgery; anticoagulant; anti-inflammatory;
KW anti-arthritic; thrombolytic; antirheumatic; antipsoriatic;
KW immunosuppressant; pancreatitis; deep vein thrombosis; psoriasis;
KW rheumatoid arthritis; myocardial infarction; transplant rejection.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO9963090-A2.
XX
PD 09-DEC-1999.
XX
PF 03-JUN-1999; 99WO-US012276.
XX
PR 03-JUN-1998; 98US-0087885P.
XX
PA (SCIO-) SCIOS INC.
XX
PI White RT, Damm D, Lesikar DD, Mcfadden K, Garrick BL, Lucas AB;
PI Pollitt NS, Lam AO;
XX
DR WPI; 2000-105699/09.
XX
PT Novel enzyme inhibitors especially used to reduce postoperative bleeding.
XX
PS Example 3; Fig 37; 151pp; English.
XX
CC The present invention describes protease inhibitors that are analogues of
CC the Kunitz protease inhibitor (KPI) domain of the amyloid precursor

```
CC   protein. The protease inhibitors can be used used to treat or prevent
CC   disorders associated with increased activity of serine proteases,
CC   specifically blood loss during surgery (particularly cardiopulmonary
CC   bypass surgery where plasma proteases are activated by contact with
CC   surfaces in the heart-lung machine), but also other conditions such as
CC   pancreatitis; deep vein thrombosis; rheumatoid arthritis; psoriasis;
CC   myocardial infarction; and transplant rejection. They are also for organ
CC   preservation and to promote wound healing. In vitro the protease
CC   inhibitors may be used to inhibit serine proteases during preparation of
CC   cell extracts. The protease inhibitors are based on a human peptide
CC   sequence so are unlikely to be immunogenic, can be produced at high
CC   levels in recombinant expression systems, and can inhibit a wide range of
CC   serine proteases. They are more potent or specific than known inhibitors.
CC   The present sequence is given in an example from the present invention
XX
SQ   Sequence 61 AA;

  Query Match             98.6%;  Score 346;  DB 3;  Length 61;
  Best Local Similarity   98.4%;  Pred. No. 3.9e-31;
  Matches   60;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 EVVREVCSEQAETGPCRAAIYHWYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMAVCGSA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||:||||||||
Db          1 EVVREVCSEQAETGPCRAAIYHWYFDVTEGKCAPFFYGGCGGNRNNFDTEEHCMAVCGSA 60

Qy         61 I 61
              |
Db         61 I 61


RESULT 10
AAY68157
ID   AAY68157 standard; protein; 61 AA.
XX
AC   AAY68157;
XX
DT   13-APR-2000  (first entry)
XX
DE   Kunitz protease inhibitor variant BG015.
XX
KW   Kunitz protease inhibitor; KPI; serine protease; kallikrein; plasmin;
KW   amyloid precursor protein; coagulation factor; blood loss; cardiant;
KW   cardiopulmonary bypass surgery; anticoagulant; anti-inflammatory;
KW   anti-arthritic; thrombolytic; antirheumatic; antipsoriatic;
KW   immunosuppressant; pancreatitis; deep vein thrombosis; psoriasis;
KW   rheumatoid arthritis; myocardial infarction; transplant rejection.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO9963090-A2.
XX
PD   09-DEC-1999.
XX
PF   03-JUN-1999;   99WO-US012276.
XX
PR   03-JUN-1998;   98US-0087885P.
XX
PA   (SCIO-) SCIOS INC.
XX
PI   White RT,  Damm D,  Lesikar DD,  Mcfadden K,  Garrick BL,  Lucas AB;
PI   Pollitt NS,  Lam AO;
XX
DR   WPI; 2000-105699/09.
XX
PT   Novel enzyme inhibitors especially used to reduce postoperative bleeding.
XX
PS   Example 4; Fig 64; 151pp; English.
XX
CC   The present invention describes protease inhibitors that are analogues of
CC   the Kunitz protease inhibitor (KPI) domain of the amyloid precursor
CC   protein. The protease inhibitors can be used used to treat or prevent
CC   disorders associated with increased activity of serine proteases,
CC   specifically blood loss during surgery (particularly cardiopulmonary
CC   bypass surgery where plasma proteases are activated by contact with
CC   surfaces in the heart-lung machine), but also other conditions such as
CC   pancreatitis; deep vein thrombosis; rheumatoid arthritis; psoriasis;
CC   myocardial infarction; and transplant rejection. They are also for organ
CC   preservation and to promote wound healing. In vitro the protease
CC   inhibitors may be used to inhibit serine proteases during preparation of
CC   cell extracts. The protease inhibitors are based on a human peptide
CC   sequence so are unlikely to be immunogenic, can be produced at high
CC   levels in recombinant expression systems, and can inhibit a wide range of
CC   serine proteases. They are more potent or specific than known inhibitors.
CC   The present sequence represents a KPI variant which is given in an
CC   example from the present invention
XX
SQ   Sequence 61 AA;

  Query Match             98.6%;  Score 346;  DB 3;  Length 61;
  Best Local Similarity   98.4%;  Pred. No. 3.9e-31;
  Matches   60;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 EVVREVCSEQAETGPCRAAIYHWYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMAVCGSA 60
              |||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Db          1 EVVREVCSEQAETGPCRALIYHWYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMAVCGSA 60

Qy         61 I 61
              |
Db         61 I 61


RESULT 11
AAY68168
ID   AAY68168 standard; protein; 61 AA.
XX
AC   AAY68168;
XX
DT   13-APR-2000  (first entry)
XX
DE   Kunitz protease inhibitor variant BG033.
XX
KW   Kunitz protease inhibitor; KPI; serine protease; kallikrein; plasmin;
KW   amyloid precursor protein; coagulation factor; blood loss; cardiant;
KW   cardiopulmonary bypass surgery; anticoagulant; anti-inflammatory;
KW   anti-arthritic; thrombolytic; antirheumatic; antipsoriatic;
KW   immunosuppressant; pancreatitis; deep vein thrombosis; psoriasis;
KW   rheumatoid arthritis; myocardial infarction; transplant rejection.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO9963090-A2.
XX
PD   09-DEC-1999.
XX
PF   03-JUN-1999;   99WO-US012276.
XX
PR   03-JUN-1998;   98US-0087885P.
XX
PA   (SCIO-) SCIOS INC.
XX
PI   White RT,  Damm D,  Lesikar DD,  Mcfadden K,  Garrick BL,  Lucas AB;
PI   Pollitt NS,  Lam AO;
XX
DR   WPI; 2000-105699/09.
XX
PT   Novel enzyme inhibitors especially used to reduce postoperative bleeding.
XX
PS   Example 4; Fig 64; 151pp; English.
XX
CC   The present invention describes protease inhibitors that are analogues of
CC   the Kunitz protease inhibitor (KPI) domain of the amyloid precursor
CC   protein. The protease inhibitors can be used used to treat or prevent
CC   disorders associated with increased activity of serine proteases,
CC   specifically blood loss during surgery (particularly cardiopulmonary
```

CC bypass surgery where plasma proteases are activated by contact with
CC surfaces in the heart-lung machine), but also other conditions such as
CC pancreatitis; deep vein thrombosis; rheumatoid arthritis; psoriasis;
CC myocardial infarction; and transplant rejection. They are also for organ
CC preservation and to promote wound healing. In vitro the protease
CC inhibitors may be used to inhibit serine proteases during preparation of
CC cell extracts. The protease inhibitors are based on a human peptide
CC sequence so are unlikely to be immunogenic, can be produced at high
CC levels in recombinant expression systems, and can inhibit a wide range of
CC serine proteases. They are more potent or specific than known inhibitors.
CC The present sequence represents a KPI variant which is given in an
CC example from the present invention
XX
SQ Sequence 61 AA;

Query Match 98.6%; Score 346; DB 3; Length 61;
Best Local Similarity 98.4%; Pred. No. 3.9e-31;
Matches 60; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 EVVREVCSEQAETGPCRAAIYHWYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMAVCGSA 60
||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1 EVVREVCSEQAEVGPCRAAIYHWYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMAVCGSA 60

Qy 61 I 61
|
Db 61 I 61

RESULT 12
AAU09319
ID AAU09319 standard; protein; 61 AA.
XX
AC AAU09319;
XX
DT 03-JAN-2002 (first entry)
XX
DE Human KPI variant, BG022.
XX
KW Human; serine protease inhibitor; Kunitz Protease Inhibitor; KPI;
KW amyloid precursor protein; kallikrein; plasmin; coagulation factor;
KW blood loss; surgery; respiratory disorder; deep vein thrombosis;
KW inflammatory bowel disease; cardiovascular disorder; haemostatic; mutant;
KW mutein; variant.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN US2001020003-A1.
XX
PD 06-SEP-2001.
XX
PF 21-JAN-1999; 99US-00234874.
XX
PR 21-JAN-1999; 99US-00234874.
XX
PA (WHIT/) WHITE R T.
PA (DAMM/) DAMM D.
PA (LESI/) LESIKAR D D.
PA (MCFA/) MCFADDEN K.
PA (GARR/) GARRICK B L.
XX
PI White RT, Damm D, Lesikar DD, Mcfadden K, Garrick BL;
XX
DR WPI; 2001-570185/64.
XX
PT New serine protease inhibitors useful in ameliorating, treating or
PT preventing clinical conditions associated with increased activity of
PT serine proteases e.g. pulmonary injury, pacreatitis, deep vein
PT thrombosis, wound healing.
XX
PS Example 4; Fig 46; 74pp; English.
XX
CC The present invention relates to serine protease inhibitor peptides.
CC These peptides which are analogues of the Kunitz Protease Inhibitor (KPI)
CC domain of amyloid precursor protein bind and inhibit the activity of
CC serine proteases such as kallikrein, plasmin, and coagulation factors
CC (e.g. factors VIIa, IXa, Xa, XIa, and XIIa). The protease inhibitors of
CC the invention are useful for treating blood loss during surgery. The
CC protease inhibitors may also be used in ameliorating, treating or
CC preventing clinical conditions associated with increased activity of
CC serine proteases, in reducing tissue damage caused by activation of the
CC proteases of the contact pathway of the blood during surgical procedures
CC such as cardiopulmonary bypass, or reducing serine protease-associated
CC peri-operative and post-operative blood loss. Examples of other clinical
CC conditions associated with increased serine protease activity for which
CC the peptides may be used as treatment includes pulmonary injury,
CC pancreatitis, allergy-induced protease release, deep vein thrombosis,
CC thrombocytopaenia, rheumatoid arthritis, adult respiratory distress
CC syndrome, chronic inflammatory bowel disease, psoriasis,
CC hyperfibrinolytic haemorrhage, organ preservation, wound healing and
CC myocardial infarction. AAU09229-AAU09339 represent human KPI variants of
CC the present invention
XX
SQ Sequence 61 AA;

Query Match 98.6%; Score 346; DB 4; Length 61;
Best Local Similarity 98.4%; Pred. No. 3.9e-31;
Matches 60; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVVREVCSEQAETGPCRAAIYHWYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMAVCGSA 60
||||||||||||||||||||||||||||||||||||||||||||||||||||:||||||||
Db 1 EVVREVCSEQAETGPCRAAIYHWYFDVTEGKCAPFFYGGCGGNRNNFDTEEHCMAVCGSA 60

Qy 61 I 61
|
Db 61 I 61

RESULT 13
AAU09317
ID AAU09317 standard; protein; 61 AA.
XX
AC AAU09317;
XX
DT 03-JAN-2002 (first entry)
XX
DE Human KPI variant, BG015.
XX
KW Human; serine protease inhibitor; Kunitz Protease Inhibitor; KPI;
KW amyloid precursor protein; kallikrein; plasmin; coagulation factor;
KW blood loss; surgery; respiratory disorder; deep vein thrombosis;
KW inflammatory bowel disease; cardiovascular disorder; haemostatic; mutant;
KW mutein; variant.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN US2001020003-A1.
XX
PD 06-SEP-2001.
XX
PF 21-JAN-1999; 99US-00234874.
XX
PR 21-JAN-1999; 99US-00234874.
XX
PA (WHIT/) WHITE R T.
PA (DAMM/) DAMM D.
PA (LESI/) LESIKAR D D.
PA (MCFA/) MCFADDEN K.
PA (GARR/) GARRICK B L.
XX
PI White RT, Damm D, Lesikar DD, Mcfadden K, Garrick BL;
XX
DR WPI; 2001-570185/64.
XX
PT New serine protease inhibitors useful in ameliorating, treating or

PT preventing clinical conditions associated with increased activity of
PT serine proteases e.g. pulmonary injury, pacreatitis, deep vein
PT thrombosis, wound healing.
XX
PS Example 4; Fig 46; 74pp; English.
XX
CC The present invention relates to serine protease inhibitor peptides.
CC These peptides which are analogues of the Kunitz Protease Inhibitor (KPI)
CC domain of amyloid precursor protein bind and inhibit the activity of
CC serine proteases such as kallikrein, plasmin, and coagulation factors
CC (e.g. factors VIIa, IXa, Xa, XIa, and XIIa). The protease inhibitors of
CC the invention are useful for treating blood loss during surgery. The
CC protease inhibitors may also be used in ameliorating, treating or
CC preventing clinical conditions associated with increased activity of
CC serine proteases, in reducing tissue damage caused by activation of the
CC proteases of the contact pathway of the blood during surgical procedures
CC such as cardiopulmonary bypass, or reducing serine protease-associated
CC peri-operative and post-operative blood loss. Examples of other clinical
CC conditions associated with increased serine protease activity for which
CC the peptides may be used as treatment includes pulmonary injury,
CC pancreatitis, allergy-induced protease release, deep vein thrombosis,
CC thrombocytopaenia, rheumatoid arthritis, adult respiratory distress
CC syndrome, chronic inflammatory bowel disease, psoriasis,
CC hyperfibrinolytic haemorrhage, organ preservation, wound healing and
CC myocardial infarction. AAU09229-AAU09339 represent human KPI variants of
CC the present invention
XX
SQ Sequence 61 AA;

Query Match 98.6%; Score 346; DB 4; Length 61;
Best Local Similarity 98.4%; Pred. No. 3.9e-31;
Matches 60; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy          1 EVVREVCSEQAETGPCRAAIYHWYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMAVCGSA 60
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Db          1 EVVREVCSEQAETGPCRALIYHWYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMAVCGSA 60

Qy         61 I 61
              |
Db         61 I 61
```

RESULT 14
AAY68049
ID AAY68049 standard; protein; 146 AA.
XX
AC AAY68049;
XX
DT 13-APR-2000 (first entry)
XX
DE Yeast mating-factor-KPI(-4-57) fusion protein sequence Fig 20.
XX
KW Kunitz protease inhibitor; KPI; serine protease; kallikrein; plasmin;
KW amyloid precursor protein; coagulation factor; blood loss; cardiant;
KW cardiopulmonary bypass surgery; anticoagulant; anti-inflammatory;
KW anti-arthritic; thrombolytic; antirheumatic; antipsoriatic;
KW immunosuppressant; pancreatitis; deep vein thrombosis; psoriasis;
KW rheumatoid arthritis; myocardial infarction; transplant rejection.
XX
OS Homo sapiens.
OS Saccharomyces cerevisiae.
OS Synthetic.
XX
PN WO9963090-A2.
XX
PD 09-DEC-1999.
XX
PF 03-JUN-1999; 99WO-US012276.
XX
PR 03-JUN-1998; 98US-0087885P.
XX
PA (SCIO-) SCIOS INC.
XX
PI White RT, Damm D, Lesikar DD, Mcfadden K, Garrick BL, Lucas AB;
PI Pollitt NS, Lam AO;
XX
DR WPI; 2000-105699/09.
DR N-PSDB; AAZ57535.
XX
PT Novel enzyme inhibitors especially used to reduce postoperative bleeding.
XX
PS Example 3; Fig 20; 151pp; English.
XX
CC The present invention describes protease inhibitors that are analogues of
CC the Kunitz protease inhibitor (KPI) domain of the amyloid precursor
CC protein. The protease inhibitors can be used used to treat or prevent
CC disorders associated with increased activity of serine proteases,
CC specifically blood loss during surgery (particularly cardiopulmonary
CC bypass surgery where plasma proteases are activated by contact with
CC surfaces in the heart-lung machine), but also other conditions such as
CC pancreatitis; deep vein thrombosis; rheumatoid arthritis; psoriasis;
CC myocardial infarction; and transplant rejection. They are also for organ
CC preservation and to promote wound healing. In vitro the protease
CC inhibitors may be used to inhibit serine proteases during preparation of
CC cell extracts. The protease inhibitors are based on a human peptide
CC sequence so are unlikely to be immunogenic, can be produced at high
CC levels in recombinant expression systems, and can inhibit a wide range of
CC serine proteases. They are more potent or specific than known inhibitors.
CC The present sequence is given in an example from the present invention
XX
SQ Sequence 146 AA;

Query Match 98.6%; Score 346; DB 3; Length 146;
Best Local Similarity 98.4%; Pred. No. 9.4e-31;
Matches 60; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 EVVREVCSEQAETGPCRAAIYHWYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMAVCGSA 60
              |||||||||||||||||||||||||||||||||||||||||||||||||||:||||||||
Db         86 EVVREVCSEQAETGPCRAAIYHWYFDVTEGKCAPFFYGGCGGNRNNFDTEEHCMAVCGSA 145

Qy         61 I 61
              |
Db        146 I 146
```

RESULT 15
AAY68057
ID AAY68057 standard; protein; 146 AA.
XX
AC AAY68057;
XX
DT 13-APR-2000 (first entry)
XX
DE Yeast mating-factor-KPI(-4-57) fusion protein sequence Fig 24.
XX
KW Kunitz protease inhibitor; KPI; serine protease; kallikrein; plasmin;
KW amyloid precursor protein; coagulation factor; blood loss; cardiant;
KW cardiopulmonary bypass surgery; anticoagulant; anti-inflammatory;
KW anti-arthritic; thrombolytic; antirheumatic; antipsoriatic;
KW immunosuppressant; pancreatitis; deep vein thrombosis; psoriasis;
KW rheumatoid arthritis; myocardial infarction; transplant rejection.
XX
OS Homo sapiens.
OS Saccharomyces cerevisiae.
OS Synthetic.
XX
PN WO9963090-A2.
XX
PD 09-DEC-1999.
XX
PF 03-JUN-1999; 99WO-US012276.
XX
PR 03-JUN-1998; 98US-0087885P.
XX
PA (SCIO-) SCIOS INC.
XX

PI White RT, Damm D, Lesikar DD, Mcfadden K, Garrick BL, Lucas AB;
PI Pollitt NS, Lam AO;
XX
DR WPI; 2000-105699/09.
DR N-PSDB; AAZ57539.
XX
PT Novel enzyme inhibitors especially used to reduce postoperative bleeding.
XX
PS Example 3; Fig 24; 151pp; English.
XX
CC The present invention describes protease inhibitors that are analogues of
CC the Kunitz protease inhibitor (KPI) domain of the amyloid precursor
CC protein. The protease inhibitors can be used used to treat or prevent
CC disorders associated with increased activity of serine proteases,
CC specifically blood loss during surgery (particularly cardiopulmonary
CC bypass surgery where plasma proteases are activated by contact with
CC surfaces in the heart-lung machine), but also other conditions such as
CC pancreatitis; deep vein thrombosis; rheumatoid arthritis; psoriasis;
CC myocardial infarction; and transplant rejection. They are also for organ
CC preservation and to promote wound healing. In vitro the protease
CC inhibitors may be used to inhibit serine proteases during preparation of
CC cell extracts. The protease inhibitors are based on a human peptide
CC sequence so are unlikely to be immunogenic, can be produced at high
CC levels in recombinant expression systems, and can inhibit a wide range of
CC serine proteases. They are more potent or specific than known inhibitors.
CC The present sequence is given in an example from the present invention
XX
SQ Sequence 146 AA;

Query Match 98.6%; Score 346; DB 3; Length 146;
Best Local Similarity 98.4%; Pred. No. 9.4e-31;
Matches 60; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy          1 EVVREVCSEQAETGPCRAAIYHWYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMAVCGSA 60
              ||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db         86 EVVREVCSEQAEVGPCRAAIYHWYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMAVCGSA 145

Qy         61 I 61
              |
Db        146 I 146
```

Search completed: April 8, 2004, 09:33:20
Job time : 55 secs

OM protein - protein search, using sw model

Run on: April 8, 2004, 09:26:35 ; Search time 23 Seconds
(without alignments)
136.921 Million cell updates/sec

Title: US-10-076-604-208
Perfect score: 351
Sequence: 1 EVVREVCSEQAETGPCRAAI.....GNRNNFDTEEYCMAVCGSAI 61

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
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5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	351	100.0	61	2	US-08-829-876-208	Sequence 208, App
2	351	100.0	61	4	US-09-234-874A-208	Sequence 208, App
3	351	100.0	61	4	US-09-234-873A-208	Sequence 208, App
4	347	98.9	61	2	US-08-829-876-218	Sequence 218, App
5	347	98.9	61	2	US-08-829-876-224	Sequence 224, App
6	347	98.9	61	4	US-09-234-874A-218	Sequence 218, App
7	347	98.9	61	4	US-09-234-874A-224	Sequence 224, App
8	347	98.9	61	4	US-09-234-873A-218	Sequence 218, App
9	347	98.9	61	4	US-09-234-873A-224	Sequence 224, App
10	346	98.6	61	2	US-08-829-876-206	Sequence 206, App
11	346	98.6	61	2	US-08-829-876-217	Sequence 217, App
12	346	98.6	61	4	US-09-234-874A-206	Sequence 206, App
13	346	98.6	61	4	US-09-234-874A-217	Sequence 217, App
14	346	98.6	61	4	US-09-234-873A-206	Sequence 206, App
15	346	98.6	61	4	US-09-234-873A-217	Sequence 217, App
16	343	97.7	61	2	US-08-829-876-173	Sequence 173, App
17	343	97.7	61	2	US-08-829-876-211	Sequence 211, App
18	343	97.7	61	4	US-09-234-874A-173	Sequence 173, App
19	343	97.7	61	4	US-09-234-874A-211	Sequence 211, App
20	343	97.7	61	4	US-09-234-873A-173	Sequence 173, App
21	343	97.7	61	4	US-09-234-873A-211	Sequence 211, App
22	343	97.7	146	2	US-08-829-876-85	Sequence 85, Appl
23	343	97.7	146	4	US-09-234-874A-85	Sequence 85, Appl
24	343	97.7	146	4	US-09-234-873A-85	Sequence 85, Appl
25	342	97.4	61	2	US-08-829-876-216	Sequence 216, App
26	342	97.4	61	2	US-08-829-876-223	Sequence 223, App
27	342	97.4	61	4	US-09-234-874A-216	Sequence 216, App
28	342	97.4	61	4	US-09-234-874A-223	Sequence 223, App
29	342	97.4	61	4	US-09-234-873A-216	Sequence 216, App
30	342	97.4	61	4	US-09-234-873A-223	Sequence 223, App
31	341	97.2	61	2	US-08-829-876-204	Sequence 204, App
32	341	97.2	61	2	US-08-829-876-215	Sequence 215, App
33	341	97.2	61	4	US-09-234-874A-204	Sequence 204, App
34	341	97.2	61	4	US-09-234-874A-215	Sequence 215, App
35	341	97.2	61	4	US-09-234-873A-204	Sequence 204, App
36	341	97.2	61	4	US-09-234-873A-215	Sequence 215, App
37	340	96.9	61	2	US-08-829-876-219	Sequence 219, App
38	340	96.9	61	4	US-09-234-874A-219	Sequence 219, App
39	340	96.9	61	4	US-09-234-873A-219	Sequence 219, App
40	339	96.6	61	2	US-08-829-876-171	Sequence 171, App
41	339	96.6	61	2	US-08-829-876-178	Sequence 178, App
42	339	96.6	61	2	US-08-829-876-220	Sequence 220, App
43	339	96.6	61	4	US-09-234-874A-171	Sequence 171, App
44	339	96.6	61	4	US-09-234-874A-178	Sequence 178, App
45	339	96.6	61	4	US-09-234-874A-220	Sequence 220, App

ALIGNMENTS

RESULT 1
US-08-829-876-208
; Sequence 208, Application US/08829876
; Patent No. 5962266
; GENERAL INFORMATION:
; APPLICANT: White, Tyler R.
; APPLICANT: Damm, Deborah
; APPLICANT: Lesikar, David D.
; APPLICANT: McFadden, Kathleen
; APPLICANT: Garrick, Brett L.
; TITLE OF INVENTION: PROTEASE INHIBITOR PEPTIDES
; NUMBER OF SEQUENCES: 228
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/829,876
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/436,555
; FILING DATE: 08-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Pelto, Don J.
; REGISTRATION NUMBER: 33,754
; REFERENCE/DOCKET NUMBER: 56324/106/SCNO
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 208:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 61 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-829-876-208

Query Match 100.0%; Score 351; DB 2; Length 61;
Best Local Similarity 100.0%; Pred. No. 8.4e-34;

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  Matches   61;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Db          1 EVVREVCSEQAETGPCRAAIYHWYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMAVCGSA 60

Qy         61 I 61
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Db         61 I 61


RESULT 2
US-09-234-874A-208
; Sequence 208, Application US/09234874A
; Patent No. 6376648
;  GENERAL INFORMATION:
;       APPLICANT: White, Tyler R.
;                  Damm, Deborah
;                  Lesikar, David D.
;                  McFadden, Kathleen
;                  Garrick, Brett L.
;       TITLE OF INVENTION: PROTEASE INHIBITOR PEPTIDES
;       NUMBER OF SEQUENCES: 228
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Foley & Lardner
;            STREET: 3000 K Street, N.W., Suite 500
;            CITY: Washington
;            STATE: D.C.
;            COUNTRY: USA
;            ZIP: 20007-5109
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/234,874A
;            FILING DATE: 11-Jun-2001
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: 08/436,555
;            FILING DATE: 08-MAY-1995
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Bent, Stephen
;            REGISTRATION NUMBER: 29,768
;            REFERENCE/DOCKET NUMBER: 056324/0106
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: (202)672-5300
;            TELEFAX: (202)672-5399
;            TELEX: 904136
;   INFORMATION FOR SEQ ID NO: 208:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 61 amino acids
;            TYPE: amino acid
;            STRANDEDNESS: single
;            TOPOLOGY: linear
;       MOLECULE TYPE: protein
;       SEQUENCE DESCRIPTION: SEQ ID NO: 208:
US-09-234-874A-208

  Query Match           100.0%;  Score 351;  DB 4;  Length 61;
  Best Local Similarity  100.0%;  Pred. No. 8.4e-34;
  Matches   61;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Db          1 EVVREVCSEQAETGPCRAAIYHWYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMAVCGSA 60

Qy         61 I 61
              |
Db         61 I 61


RESULT 3
US-09-234-873A-208
; Sequence 208, Application US/09234873A
; Patent No. 6613890
;  GENERAL INFORMATION:
;       APPLICANT: White, Tyler R.
;                  Damm, Deborah
;                  Lesikar, David D.
;                  McFadden, Kathleen
;                  Garrick, Brett L.
;       TITLE OF INVENTION: PROTEASE INHIBITOR PEPTIDES
;       NUMBER OF SEQUENCES: 228
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Foley & Lardner
;            STREET: 3000 K Street, N.W., Suite 500
;            CITY: Washington
;            STATE: D.C.
;            COUNTRY: USA
;            ZIP: 20007-5109
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/234,873A
;            FILING DATE: 21-Jan-1999
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: 08/829,876
;            FILING DATE: 02-APR-1997
;            APPLICATION NUMBER: 08/436,555
;            FILING DATE: 08-MAY-1995
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Bent, Stephen
;            REGISTRATION NUMBER: 29,768
;            REFERENCE/DOCKET NUMBER: 056324/0116
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: (202)672-5300
;            TELEFAX: (202)672-5399
;            TELEX: 904136
;   INFORMATION FOR SEQ ID NO: 208:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 61 amino acids
;            TYPE: amino acid
;            STRANDEDNESS: single
;            TOPOLOGY: linear
;       MOLECULE TYPE: protein
;       SEQUENCE DESCRIPTION: SEQ ID NO: 208:
US-09-234-873A-208

  Query Match           100.0%;  Score 351;  DB 4;  Length 61;
  Best Local Similarity  100.0%;  Pred. No. 8.4e-34;
  Matches   61;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 EVVREVCSEQAETGPCRAAIYHWYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMAVCGSA 60
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Db          1 EVVREVCSEQAETGPCRAAIYHWYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMAVCGSA 60

Qy         61 I 61
              |
Db         61 I 61


RESULT 4
US-08-829-876-218
; Sequence 218, Application US/08829876
; Patent No. 5962266
;  GENERAL INFORMATION:
;    APPLICANT:  White, Tyler R.
;    APPLICANT:  Damm, Deborah
;    APPLICANT:  Lesikar, David D.
;    APPLICANT:  McFadden, Kathleen
;    APPLICANT:  Garrick, Brett L.
;    TITLE OF INVENTION:  PROTEASE INHIBITOR PEPTIDES
```

```
;    NUMBER OF SEQUENCES:  228
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Foley & Lardner
;      STREET:  3000 K Street, N.W., Suite 500
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20007-5109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/829,876
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/436,555
;      FILING DATE:  08-MAY-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Pelto, Don J.
;      REGISTRATION NUMBER:  33,754
;      REFERENCE/DOCKET NUMBER:  56324/106/SCNO
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202)672-5300
;      TELEFAX:  (202)672-5399
;      TELEX:  904136
;  INFORMATION FOR SEQ ID NO:  218:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  61 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-829-876-218

  Query Match             98.9%;  Score 347;  DB 2;  Length 61;
  Best Local Similarity   98.4%;  Pred. No. 2.4e-33;
  Matches   60;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 EVVREVCSEQAETGPCRAAIYHWYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMAVCGSA 60
              ||||||||||||:||||||||||||||||||||||||||||||||||||||||||||||
Db          1 EVVREVCSEQAESGPCRAAIYHWYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMAVCGSA 60

Qy         61 I 61
              |
Db         61 I 61


RESULT 5
US-08-829-876-224
; Sequence 224, Application US/08829876
; Patent No. 5962266
;  GENERAL INFORMATION:
;    APPLICANT:  White, Tyler R.
;    APPLICANT:  Damm, Deborah
;    APPLICANT:  Lesikar, David D.
;    APPLICANT:  McFadden, Kathleen
;    APPLICANT:  Garrick, Brett L.
;    TITLE OF INVENTION:  PROTEASE INHIBITOR PEPTIDES
;    NUMBER OF SEQUENCES:  228
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Foley & Lardner
;      STREET:  3000 K Street, N.W., Suite 500
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20007-5109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/829,876
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/436,555
;      FILING DATE:  08-MAY-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Pelto, Don J.
;      REGISTRATION NUMBER:  33,754
;      REFERENCE/DOCKET NUMBER:  56324/106/SCNO
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202)672-5300
;      TELEFAX:  (202)672-5399
;      TELEX:  904136
;  INFORMATION FOR SEQ ID NO:  224:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  61 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-829-876-224

  Query Match             98.9%;  Score 347;  DB 2;  Length 61;
  Best Local Similarity   98.4%;  Pred. No. 2.4e-33;
  Matches   60;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

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Db          1 EVVREVCSEQAETGPCRGAIYHWYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMAVCGSA 60

Qy         61 I 61
              |
Db         61 I 61


RESULT 6
US-09-234-874A-218
; Sequence 218, Application US/09234874A
; Patent No. 6376648
;  GENERAL INFORMATION:
;       APPLICANT: White, Tyler R.
;                  Damm, Deborah
;                  Lesikar, David D.
;                  McFadden, Kathleen
;                  Garrick, Brett L.
;       TITLE OF INVENTION: PROTEASE INHIBITOR PEPTIDES
;       NUMBER OF SEQUENCES: 228
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Foley & Lardner
;            STREET: 3000 K Street, N.W., Suite 500
;            CITY: Washington
;            STATE: D.C.
;            COUNTRY: USA
;            ZIP: 20007-5109
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/234,874A
;            FILING DATE: 11-Jun-2001
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: 08/436,555
;            FILING DATE: 08-MAY-1995
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Bent, Stephen
;            REGISTRATION NUMBER: 29,768
;            REFERENCE/DOCKET NUMBER: 056324/0106
;       TELECOMMUNICATION INFORMATION:
```

```
;             TELEPHONE: (202)672-5300
;             TELEFAX: (202)672-5399
;             TELEX: 904136
;    INFORMATION FOR SEQ ID NO: 218:
;         SEQUENCE CHARACTERISTICS:
;             LENGTH: 61 amino acids
;             TYPE: amino acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;         MOLECULE TYPE: protein
;         SEQUENCE DESCRIPTION: SEQ ID NO: 218:
US-09-234-874A-218

  Query Match             98.9%;  Score 347;  DB 4;  Length 61;
  Best Local Similarity   98.4%;  Pred. No. 2.4e-33;
  Matches   60;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

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Db          1 EVVREVCSEQAESGPCRAAIYHWYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMAVCGSA 60

Qy         61 I 61
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Db         61 I 61


RESULT 7
US-09-234-874A-224
; Sequence 224, Application US/09234874A
; Patent No. 6376648
;   GENERAL INFORMATION:
;         APPLICANT: White, Tyler R.
;                    Damm, Deborah
;                    Lesikar, David D.
;                    McFadden, Kathleen
;                    Garrick, Brett L.
;         TITLE OF INVENTION: PROTEASE INHIBITOR PEPTIDES
;         NUMBER OF SEQUENCES: 228
;         CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Foley & Lardner
;             STREET: 3000 K Street, N.W., Suite 500
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20007-5109
;         COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;         CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/234,874A
;             FILING DATE: 11-Jun-2001
;         PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 08/436,555
;             FILING DATE: 08-MAY-1995
;         ATTORNEY/AGENT INFORMATION:
;             NAME: Bent, Stephen
;             REGISTRATION NUMBER: 29,768
;             REFERENCE/DOCKET NUMBER: 056324/0106
;         TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (202)672-5300
;             TELEFAX: (202)672-5399
;             TELEX: 904136
;    INFORMATION FOR SEQ ID NO: 224:
;         SEQUENCE CHARACTERISTICS:
;             LENGTH: 61 amino acids
;             TYPE: amino acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;         MOLECULE TYPE: protein
;         SEQUENCE DESCRIPTION: SEQ ID NO: 224:
US-09-234-874A-224

  Query Match             98.9%;  Score 347;  DB 4;  Length 61;
  Best Local Similarity   98.4%;  Pred. No. 2.4e-33;
  Matches   60;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 EVVREVCSEQAETGPCRAAIYHWYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMAVCGSA 60
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Db          1 EVVREVCSEQAETGPCRGAIYHWYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMAVCGSA 60

Qy         61 I 61
              |
Db         61 I 61


RESULT 8
US-09-234-873A-218
; Sequence 218, Application US/09234873A
; Patent No. 6613890
;   GENERAL INFORMATION:
;         APPLICANT: White, Tyler R.
;                    Damm, Deborah
;                    Lesikar, David D.
;                    McFadden, Kathleen
;                    Garrick, Brett L.
;         TITLE OF INVENTION: PROTEASE INHIBITOR PEPTIDES
;         NUMBER OF SEQUENCES: 228
;         CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Foley & Lardner
;             STREET: 3000 K Street, N.W., Suite 500
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20007-5109
;         COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;         CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/234,873A
;             FILING DATE: 21-Jan-1999
;         PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 08/829,876
;             FILING DATE: 02-APR-1997
;             APPLICATION NUMBER: 08/436,555
;             FILING DATE: 08-MAY-1995
;         ATTORNEY/AGENT INFORMATION:
;             NAME: Bent, Stephen
;             REGISTRATION NUMBER: 29,768
;             REFERENCE/DOCKET NUMBER: 056324/0116
;         TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (202)672-5300
;             TELEFAX: (202)672-5399
;             TELEX: 904136
;    INFORMATION FOR SEQ ID NO: 218:
;         SEQUENCE CHARACTERISTICS:
;             LENGTH: 61 amino acids
;             TYPE: amino acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;         MOLECULE TYPE: protein
;         SEQUENCE DESCRIPTION: SEQ ID NO: 218:
US-09-234-873A-218

  Query Match             98.9%;  Score 347;  DB 4;  Length 61;
  Best Local Similarity   98.4%;  Pred. No. 2.4e-33;
  Matches   60;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 EVVREVCSEQAETGPCRAAIYHWYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMAVCGSA 60
              ||||||||||||:||||||||||||||||||||||||||||||||||||||||||||||
Db          1 EVVREVCSEQAESGPCRAAIYHWYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMAVCGSA 60

Qy         61 I 61
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Db          61 I 61


RESULT 9
US-09-234-873A-224
; Sequence 224, Application US/09234873A
; Patent No. 6613890
;  GENERAL INFORMATION:
;       APPLICANT: White, Tyler R.
;                  Damm, Deborah
;                  Lesikar, David D.
;                  McFadden, Kathleen
;                  Garrick, Brett L.
;       TITLE OF INVENTION: PROTEASE INHIBITOR PEPTIDES
;       NUMBER OF SEQUENCES: 228
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Foley & Lardner
;            STREET: 3000 K Street, N.W., Suite 500
;            CITY: Washington
;            STATE: D.C.
;            COUNTRY: USA
;            ZIP: 20007-5109
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/234,873A
;            FILING DATE: 21-Jan-1999
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: 08/829,876
;            FILING DATE: 02-APR-1997
;            APPLICATION NUMBER: 08/436,555
;            FILING DATE: 08-MAY-1995
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Bent, Stephen
;            REGISTRATION NUMBER: 29,768
;            REFERENCE/DOCKET NUMBER: 056324/0116
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: (202)672-5300
;            TELEFAX: (202)672-5399
;            TELEX: 904136
;   INFORMATION FOR SEQ ID NO: 224:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 61 amino acids
;            TYPE: amino acid
;            STRANDEDNESS: single
;            TOPOLOGY: linear
;       MOLECULE TYPE: protein
;       SEQUENCE DESCRIPTION: SEQ ID NO: 224:
US-09-234-873A-224

  Query Match             98.9%;  Score 347;  DB 4;  Length 61;
  Best Local Similarity   98.4%;  Pred. No. 2.4e-33;
  Matches   60;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 EVVREVCSEQAETGPCRAAIYHWYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMAVCGSA 60
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Db          1 EVVREVCSEQAETGPCRGAIYHWYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMAVCGSA 60

Qy         61 I 61
              |
Db         61 I 61


RESULT 10
US-08-829-876-206
; Sequence 206, Application US/08829876
; Patent No. 5962266
;  GENERAL INFORMATION:
;    APPLICANT:  White, Tyler R.
;    APPLICANT:  Damm, Deborah
;    APPLICANT:  Lesikar, David D.
;    APPLICANT:  McFadden, Kathleen
;    APPLICANT:  Garrick, Brett L.
;    TITLE OF INVENTION:  PROTEASE INHIBITOR PEPTIDES
;    NUMBER OF SEQUENCES:  228
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Foley & Lardner
;      STREET:  3000 K Street, N.W., Suite 500
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20007-5109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/829,876
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/436,555
;      FILING DATE:  08-MAY-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Pelto, Don J.
;      REGISTRATION NUMBER:  33,754
;      REFERENCE/DOCKET NUMBER:  56324/106/SCNO
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202)672-5300
;      TELEFAX:  (202)672-5399
;      TELEX:  904136
;  INFORMATION FOR SEQ ID NO:  206:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  61 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-829-876-206

  Query Match             98.6%;  Score 346;  DB 2;  Length 61;
  Best Local Similarity   98.4%;  Pred. No. 3.2e-33;
  Matches   60;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

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Db          1 EVVREVCSEQAETGPCRALIYHWYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMAVCGSA 60

Qy         61 I 61
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Db         61 I 61


RESULT 11
US-08-829-876-217
; Sequence 217, Application US/08829876
; Patent No. 5962266
;  GENERAL INFORMATION:
;    APPLICANT:  White, Tyler R.
;    APPLICANT:  Damm, Deborah
;    APPLICANT:  Lesikar, David D.
;    APPLICANT:  McFadden, Kathleen
;    APPLICANT:  Garrick, Brett L.
;    TITLE OF INVENTION:  PROTEASE INHIBITOR PEPTIDES
;    NUMBER OF SEQUENCES:  228
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Foley & Lardner
;      STREET:  3000 K Street, N.W., Suite 500
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
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;       ZIP: 20007-5109
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE: Floppy disk
;       COMPUTER: IBM PC compatible
;       OPERATING SYSTEM: PC-DOS/MS-DOS
;       SOFTWARE: PatentIn Release #1.0, Version #1.30
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER: US/08/829,876
;       FILING DATE:
;       CLASSIFICATION:
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER: US 08/436,555
;       FILING DATE: 08-MAY-1995
;     ATTORNEY/AGENT INFORMATION:
;       NAME: Pelto, Don J.
;       REGISTRATION NUMBER: 33,754
;       REFERENCE/DOCKET NUMBER: 56324/106/SCNO
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE: (202)672-5300
;       TELEFAX: (202)672-5399
;       TELEX: 904136
;   INFORMATION FOR SEQ ID NO: 217:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH: 61 amino acids
;       TYPE: amino acid
;       STRANDEDNESS: single
;       TOPOLOGY: linear
;     MOLECULE TYPE: protein
US-08-829-876-217

  Query Match             98.6%;  Score 346;  DB 2;  Length 61;
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  Matches   60;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

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Db         61 I 61


RESULT 12
US-09-234-874A-206
; Sequence 206, Application US/09234874A
; Patent No. 6376648
;   GENERAL INFORMATION:
;       APPLICANT: White, Tyler R.
;                  Damm, Deborah
;                  Lesikar, David D.
;                  McFadden, Kathleen
;                  Garrick, Brett L.
;       TITLE OF INVENTION: PROTEASE INHIBITOR PEPTIDES
;       NUMBER OF SEQUENCES: 228
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Foley & Lardner
;            STREET: 3000 K Street, N.W., Suite 500
;            CITY: Washington
;            STATE: D.C.
;            COUNTRY: USA
;            ZIP: 20007-5109
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/234,874A
;            FILING DATE: 11-Jun-2001
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: 08/436,555
;            FILING DATE: 08-MAY-1995
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Bent, Stephen
;            REGISTRATION NUMBER: 29,768
;            REFERENCE/DOCKET NUMBER: 056324/0106
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: (202)672-5300
;            TELEFAX: (202)672-5399
;            TELEX: 904136
;   INFORMATION FOR SEQ ID NO: 206:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 61 amino acids
;            TYPE: amino acid
;            STRANDEDNESS: single
;            TOPOLOGY: linear
;       MOLECULE TYPE: protein
;       SEQUENCE DESCRIPTION: SEQ ID NO: 206:
US-09-234-874A-206

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  Best Local Similarity   98.4%;  Pred. No. 3.2e-33;
  Matches   60;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

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Qy         61 I 61
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Db         61 I 61


RESULT 13
US-09-234-874A-217
; Sequence 217, Application US/09234874A
; Patent No. 6376648
;   GENERAL INFORMATION:
;       APPLICANT: White, Tyler R.
;                  Damm, Deborah
;                  Lesikar, David D.
;                  McFadden, Kathleen
;                  Garrick, Brett L.
;       TITLE OF INVENTION: PROTEASE INHIBITOR PEPTIDES
;       NUMBER OF SEQUENCES: 228
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Foley & Lardner
;            STREET: 3000 K Street, N.W., Suite 500
;            CITY: Washington
;            STATE: D.C.
;            COUNTRY: USA
;            ZIP: 20007-5109
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
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;            APPLICATION NUMBER: US/09/234,874A
;            FILING DATE: 11-Jun-2001
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: 08/436,555
;            FILING DATE: 08-MAY-1995
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Bent, Stephen
;            REGISTRATION NUMBER: 29,768
;            REFERENCE/DOCKET NUMBER: 056324/0106
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: (202)672-5300
;            TELEFAX: (202)672-5399
;            TELEX: 904136
;   INFORMATION FOR SEQ ID NO: 217:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 61 amino acids
;            TYPE: amino acid
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;            STRANDEDNESS: single
;            TOPOLOGY: linear
;        MOLECULE TYPE: protein
;        SEQUENCE DESCRIPTION: SEQ ID NO: 217:
US-09-234-874A-217

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  Best Local Similarity   98.4%;  Pred. No. 3.2e-33;
  Matches   60;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

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Qy         61 I 61
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Db         61 I 61


RESULT 14
US-09-234-873A-206
; Sequence 206, Application US/09234873A
; Patent No. 6613890
;   GENERAL INFORMATION:
;        APPLICANT: White, Tyler R.
;                   Damm, Deborah
;                   Lesikar, David D.
;                   McFadden, Kathleen
;                   Garrick, Brett L.
;        TITLE OF INVENTION: PROTEASE INHIBITOR PEPTIDES
;        NUMBER OF SEQUENCES: 228
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Foley & Lardner
;             STREET: 3000 K Street, N.W., Suite 500
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20007-5109
;        COMPUTER READABLE FORM:
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;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/234,873A
;             FILING DATE: 21-Jan-1999
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 08/829,876
;             FILING DATE: 02-APR-1997
;             APPLICATION NUMBER: 08/436,555
;             FILING DATE: 08-MAY-1995
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Bent, Stephen
;             REGISTRATION NUMBER: 29,768
;             REFERENCE/DOCKET NUMBER: 056324/0116
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (202)672-5300
;             TELEFAX: (202)672-5399
;             TELEX: 904136
;   INFORMATION FOR SEQ ID NO: 206:
;        SEQUENCE CHARACTERISTICS:
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;        SEQUENCE DESCRIPTION: SEQ ID NO: 206:
US-09-234-873A-206

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Db          1 EVVREVCSEQAETGPCRALIYHWYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMAVCGSA 60

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Db         61 I 61


RESULT 15
US-09-234-873A-217
; Sequence 217, Application US/09234873A
; Patent No. 6613890
;   GENERAL INFORMATION:
;        APPLICANT: White, Tyler R.
;                   Damm, Deborah
;                   Lesikar, David D.
;                   McFadden, Kathleen
;                   Garrick, Brett L.
;        TITLE OF INVENTION: PROTEASE INHIBITOR PEPTIDES
;        NUMBER OF SEQUENCES: 228
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Foley & Lardner
;             STREET: 3000 K Street, N.W., Suite 500
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20007-5109
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
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;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/234,873A
;             FILING DATE: 21-Jan-1999
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 08/829,876
;             FILING DATE: 02-APR-1997
;             APPLICATION NUMBER: 08/436,555
;             FILING DATE: 08-MAY-1995
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Bent, Stephen
;             REGISTRATION NUMBER: 29,768
;             REFERENCE/DOCKET NUMBER: 056324/0116
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (202)672-5300
;             TELEFAX: (202)672-5399
;             TELEX: 904136
;   INFORMATION FOR SEQ ID NO: 217:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 61 amino acids
;             TYPE: amino acid
;             STRANDEDNESS: single
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US-09-234-873A-217

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Db         61 I 61


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OM protein - protein search, using sw model

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Title: US-10-076-604-208
Perfect score: 351
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
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2	347	98.9	61	14	US-10-076-604-218	Sequence 218, App
3	347	98.9	61	14	US-10-076-604-224	Sequence 224, App
4	346	98.6	61	14	US-10-076-604-206	Sequence 206, App
5	346	98.6	61	14	US-10-076-604-217	Sequence 217, App
6	343	97.7	61	14	US-10-076-604-173	Sequence 173, App
7	343	97.7	61	14	US-10-076-604-211	Sequence 211, App
8	343	97.7	146	14	US-10-076-604-85	Sequence 85, Appl
9	342	97.4	61	14	US-10-076-604-216	Sequence 216, App
10	342	97.4	61	14	US-10-076-604-223	Sequence 223, App
11	341	97.2	61	14	US-10-076-604-204	Sequence 204, App
12	341	97.2	61	14	US-10-076-604-215	Sequence 215, App
13	340	96.9	61	14	US-10-076-604-219	Sequence 219, App
14	339	96.6	61	14	US-10-076-604-171	Sequence 171, App
15	339	96.6	61	14	US-10-076-604-178	Sequence 178, App
16	339	96.6	61	14	US-10-076-604-220	Sequence 220, App
17	339	96.6	146	14	US-10-076-604-107	Sequence 107, App
18	338	96.3	61	14	US-10-076-604-131	Sequence 131, App
19	338	96.3	61	14	US-10-076-604-172	Sequence 172, App
20	338	96.3	61	14	US-10-076-604-174	Sequence 174, App
21	338	96.3	61	14	US-10-076-604-209	Sequence 209, App
22	338	96.3	61	14	US-10-076-604-221	Sequence 221, App
23	338	96.3	146	14	US-10-076-604-83	Sequence 83, Appl
24	338	96.3	146	14	US-10-076-604-89	Sequence 89, Appl
25	337	96.0	61	14	US-10-076-604-139	Sequence 139, App
26	337	96.0	61	14	US-10-076-604-198	Sequence 198, App
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28	337	96.0	61	14	US-10-076-604-210	Sequence 210, App
29	335	95.4	61	14	US-10-076-604-222	Sequence 222, App
30	334	95.2	61	14	US-10-076-604-117	Sequence 117, App
31	334	95.2	61	14	US-10-076-604-130	Sequence 130, App
32	334	95.2	61	14	US-10-076-604-177	Sequence 177, App
33	334	95.2	61	14	US-10-076-604-179	Sequence 179, App
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35	333	94.9	61	14	US-10-076-604-132	Sequence 132, App
36	333	94.9	61	14	US-10-076-604-134	Sequence 134, App
37	332	94.6	61	14	US-10-076-604-181	Sequence 181, App
38	332	94.6	61	14	US-10-076-604-196	Sequence 196, App
39	332	94.6	61	14	US-10-076-604-205	Sequence 205, App
40	331	94.3	61	14	US-10-076-604-120	Sequence 120, App
41	331	94.3	61	14	US-10-076-604-186	Sequence 186, App
42	331	94.3	61	14	US-10-076-604-188	Sequence 188, App
43	331	94.3	61	14	US-10-076-604-212	Sequence 212, App
44	331	94.3	146	14	US-10-076-604-93	Sequence 93, Appl
45	330	94.0	61	14	US-10-076-604-121	Sequence 121, App

ALIGNMENTS

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RESULT 1
US-10-076-604-208
; Sequence 208, Application US/10076604
; Publication No. US20030114372A1
;  GENERAL INFORMATION:
;       APPLICANT: White, Tyler R.
;                  Damm, Deborah
;                  Lesikar, David D.
;                  McFadden, Kathleen
;                  Garrick, Brett L.
;       TITLE OF INVENTION: PROTEASE INHIBITOR PEPTIDES
;       NUMBER OF SEQUENCES: 228
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Foley & Lardner
;            STREET: 3000 K Street, N.W., Suite 500
;            CITY: Washington
;            STATE: D.C.
;            COUNTRY: USA
;            ZIP: 20007-5109
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/10/076,604
;            FILING DATE: 19-Feb-2002
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: US/09/201,715
;            FILING DATE: 01-Dec-1998
;            APPLICATION NUMBER: US 08/436,555
;            FILING DATE: 08-MAY-1995
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Pelto, Don J.
;            REGISTRATION NUMBER: 33,754
;            REFERENCE/DOCKET NUMBER: 56324/117
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: (202)672-5300
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;            TELEFAX: (202)672-5399
;            TELEX: 904136
;   INFORMATION FOR SEQ ID NO: 208:
;        SEQUENCE CHARACTERISTICS:
;            LENGTH: 61 amino acids
;            TYPE: amino acid
;            STRANDEDNESS: single
;            TOPOLOGY: linear
;        MOLECULE TYPE: protein
;        SEQUENCE DESCRIPTION: SEQ ID NO: 208:
US-10-076-604-208

  Query Match            100.0%;  Score 351;  DB 14;  Length 61;
  Best Local Similarity  100.0%;  Pred. No. 1.2e-35;
  Matches   61;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Qy         61 I 61
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Db         61 I 61


RESULT 2
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; Sequence 218, Application US/10076604
; Publication No. US20030114372A1
;   GENERAL INFORMATION:
;        APPLICANT: White, Tyler R.
;                   Damm, Deborah
;                   Lesikar, David D.
;                   McFadden, Kathleen
;                   Garrick, Brett L.
;        TITLE OF INVENTION: PROTEASE INHIBITOR PEPTIDES
;        NUMBER OF SEQUENCES: 228
;        CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Foley & Lardner
;            STREET: 3000 K Street, N.W., Suite 500
;            CITY: Washington
;            STATE: D.C.
;            COUNTRY: USA
;            ZIP: 20007-5109
;        COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/10/076,604
;            FILING DATE: 19-Feb-2002
;        PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: US/09/201,715
;            FILING DATE: 01-Dec-1998
;            APPLICATION NUMBER: US 08/436,555
;            FILING DATE: 08-MAY-1995
;        ATTORNEY/AGENT INFORMATION:
;            NAME: Pelto, Don J.
;            REGISTRATION NUMBER: 33,754
;            REFERENCE/DOCKET NUMBER: 56324/117
;        TELECOMMUNICATION INFORMATION:
;            TELEPHONE: (202)672-5300
;            TELEFAX: (202)672-5399
;            TELEX: 904136
;   INFORMATION FOR SEQ ID NO: 218:
;        SEQUENCE CHARACTERISTICS:
;            LENGTH: 61 amino acids
;            TYPE: amino acid
;            STRANDEDNESS: single
;            TOPOLOGY: linear
;        MOLECULE TYPE: protein
;        SEQUENCE DESCRIPTION: SEQ ID NO: 218:
US-10-076-604-218

  Query Match            98.9%;  Score 347;  DB 14;  Length 61;
  Best Local Similarity  98.4%;  Pred. No. 3.6e-35;
  Matches   60;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 EVVREVCSEQAETGPCRAAIYHWYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMAVCGSA 60
              ||||||||||||:||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 EVVREVCSEQAESGPCRAAIYHWYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMAVCGSA 60

Qy         61 I 61
              |
Db         61 I 61


RESULT 3
US-10-076-604-224
; Sequence 224, Application US/10076604
; Publication No. US20030114372A1
;   GENERAL INFORMATION:
;        APPLICANT: White, Tyler R.
;                   Damm, Deborah
;                   Lesikar, David D.
;                   McFadden, Kathleen
;                   Garrick, Brett L.
;        TITLE OF INVENTION: PROTEASE INHIBITOR PEPTIDES
;        NUMBER OF SEQUENCES: 228
;        CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Foley & Lardner
;            STREET: 3000 K Street, N.W., Suite 500
;            CITY: Washington
;            STATE: D.C.
;            COUNTRY: USA
;            ZIP: 20007-5109
;        COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/10/076,604
;            FILING DATE: 19-Feb-2002
;        PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: US/09/201,715
;            FILING DATE: 01-Dec-1998
;            APPLICATION NUMBER: US 08/436,555
;            FILING DATE: 08-MAY-1995
;        ATTORNEY/AGENT INFORMATION:
;            NAME: Pelto, Don J.
;            REGISTRATION NUMBER: 33,754
;            REFERENCE/DOCKET NUMBER: 56324/117
;        TELECOMMUNICATION INFORMATION:
;            TELEPHONE: (202)672-5300
;            TELEFAX: (202)672-5399
;            TELEX: 904136
;   INFORMATION FOR SEQ ID NO: 224:
;        SEQUENCE CHARACTERISTICS:
;            LENGTH: 61 amino acids
;            TYPE: amino acid
;            STRANDEDNESS: single
;            TOPOLOGY: linear
;        MOLECULE TYPE: protein
;        SEQUENCE DESCRIPTION: SEQ ID NO: 224:
US-10-076-604-224

  Query Match            98.9%;  Score 347;  DB 14;  Length 61;
  Best Local Similarity  98.4%;  Pred. No. 3.6e-35;
  Matches   60;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 EVVREVCSEQAETGPCRAAIYHWYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMAVCGSA 60
              |||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db          1 EVVREVCSEQAETGPCRGAIYHWYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMAVCGSA 60
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Qy          61 I 61
               |
Db          61 I 61


RESULT 4
US-10-076-604-206
; Sequence 206, Application US/10076604
; Publication No. US20030114372A1
;   GENERAL INFORMATION:
;        APPLICANT: White, Tyler R.
;                   Damm, Deborah
;                   Lesikar, David D.
;                   McFadden, Kathleen
;                   Garrick, Brett L.
;        TITLE OF INVENTION: PROTEASE INHIBITOR PEPTIDES
;        NUMBER OF SEQUENCES: 228
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Foley & Lardner
;             STREET: 3000 K Street, N.W., Suite 500
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20007-5109
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/076,604
;             FILING DATE: 19-Feb-2002
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/09/201,715
;             FILING DATE: 01-Dec-1998
;             APPLICATION NUMBER: US 08/436,555
;             FILING DATE: 08-MAY-1995
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Pelto, Don J.
;             REGISTRATION NUMBER: 33,754
;             REFERENCE/DOCKET NUMBER: 56324/117
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (202)672-5300
;             TELEFAX: (202)672-5399
;             TELEX: 904136
;   INFORMATION FOR SEQ ID NO: 206:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 61 amino acids
;             TYPE: amino acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: protein
;        SEQUENCE DESCRIPTION: SEQ ID NO: 206:
US-10-076-604-206

  Query Match             98.6%;  Score 346;  DB 14;  Length 61;
  Best Local Similarity   98.4%;  Pred. No. 4.8e-35;
  Matches   60;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy           1 EVVREVCSEQAETGPCRAAIYHWYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMAVCGSA 60
               |||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Db           1 EVVREVCSEQAETGPCRALIYHWYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMAVCGSA 60

Qy          61 I 61
               |
Db          61 I 61


RESULT 5
US-10-076-604-217
; Sequence 217, Application US/10076604
; Publication No. US20030114372A1
;   GENERAL INFORMATION:
;        APPLICANT: White, Tyler R.
;                   Damm, Deborah
;                   Lesikar, David D.
;                   McFadden, Kathleen
;                   Garrick, Brett L.
;        TITLE OF INVENTION: PROTEASE INHIBITOR PEPTIDES
;        NUMBER OF SEQUENCES: 228
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Foley & Lardner
;             STREET: 3000 K Street, N.W., Suite 500
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20007-5109
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/076,604
;             FILING DATE: 19-Feb-2002
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/09/201,715
;             FILING DATE: 01-Dec-1998
;             APPLICATION NUMBER: US 08/436,555
;             FILING DATE: 08-MAY-1995
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Pelto, Don J.
;             REGISTRATION NUMBER: 33,754
;             REFERENCE/DOCKET NUMBER: 56324/117
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (202)672-5300
;             TELEFAX: (202)672-5399
;             TELEX: 904136
;   INFORMATION FOR SEQ ID NO: 217:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 61 amino acids
;             TYPE: amino acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: protein
;        SEQUENCE DESCRIPTION: SEQ ID NO: 217:
US-10-076-604-217

  Query Match             98.6%;  Score 346;  DB 14;  Length 61;
  Best Local Similarity   98.4%;  Pred. No. 4.8e-35;
  Matches   60;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy           1 EVVREVCSEQAETGPCRAAIYHWYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMAVCGSA 60
               |||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Db           1 EVVREVCSEQAEVGPCRAAIYHWYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMAVCGSA 60

Qy          61 I 61
               |
Db          61 I 61


RESULT 6
US-10-076-604-173
; Sequence 173, Application US/10076604
; Publication No. US20030114372A1
;   GENERAL INFORMATION:
;        APPLICANT: White, Tyler R.
;                   Damm, Deborah
;                   Lesikar, David D.
;                   McFadden, Kathleen
;                   Garrick, Brett L.
;        TITLE OF INVENTION: PROTEASE INHIBITOR PEPTIDES
;        NUMBER OF SEQUENCES: 228
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Foley & Lardner
;             STREET: 3000 K Street, N.W., Suite 500
```

```
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20007-5109
;       COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/076,604
;             FILING DATE: 19-Feb-2002
;       PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/09/201,715
;             FILING DATE: 01-Dec-1998
;             APPLICATION NUMBER: US 08/436,555
;             FILING DATE: 08-MAY-1995
;       ATTORNEY/AGENT INFORMATION:
;             NAME: Pelto, Don J.
;             REGISTRATION NUMBER: 33,754
;             REFERENCE/DOCKET NUMBER: 56324/117
;       TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (202)672-5300
;             TELEFAX: (202)672-5399
;             TELEX: 904136
;   INFORMATION FOR SEQ ID NO: 173:
;       SEQUENCE CHARACTERISTICS:
;             LENGTH: 61 amino acids
;             TYPE: amino acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;       MOLECULE TYPE: protein
;       SEQUENCE DESCRIPTION: SEQ ID NO: 173:
US-10-076-604-173

  Query Match             97.7%;  Score 343;  DB 14;  Length 61;
  Best Local Similarity   98.4%;  Pred. No. 1.1e-34;
  Matches   60;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 EVVREVCSEQAETGPCRAAIYHWYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMAVCGSA 60
              |||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db          1 EVVREVCSEQAETGPCRAAIYRWYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMAVCGSA 60

Qy         61 I 61
              |
Db         61 I 61


RESULT 7
US-10-076-604-211
; Sequence 211, Application US/10076604
; Publication No. US20030114372A1
;   GENERAL INFORMATION:
;       APPLICANT: White, Tyler R.
;                  Damm, Deborah
;                  Lesikar, David D.
;                  McFadden, Kathleen
;                  Garrick, Brett L.
;       TITLE OF INVENTION: PROTEASE INHIBITOR PEPTIDES
;       NUMBER OF SEQUENCES: 228
;       CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Foley & Lardner
;             STREET: 3000 K Street, N.W., Suite 500
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20007-5109
;       COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/076,604
;             FILING DATE: 19-Feb-2002
;       PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/09/201,715
;             FILING DATE: 01-Dec-1998
;             APPLICATION NUMBER: US 08/436,555
;             FILING DATE: 08-MAY-1995
;       ATTORNEY/AGENT INFORMATION:
;             NAME: Pelto, Don J.
;             REGISTRATION NUMBER: 33,754
;             REFERENCE/DOCKET NUMBER: 56324/117
;       TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (202)672-5300
;             TELEFAX: (202)672-5399
;             TELEX: 904136
;   INFORMATION FOR SEQ ID NO: 211:
;       SEQUENCE CHARACTERISTICS:
;             LENGTH: 61 amino acids
;             TYPE: amino acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;       MOLECULE TYPE: protein
;       SEQUENCE DESCRIPTION: SEQ ID NO: 211:
US-10-076-604-211

  Query Match             97.7%;  Score 343;  DB 14;  Length 61;
  Best Local Similarity   98.4%;  Pred. No. 1.1e-34;
  Matches   60;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 EVVREVCSEQAETGPCRAAIYHWYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMAVCGSA 60
              |||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db          1 EVVREVCSEQAETGPCRAAIQHWYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMAVCGSA 60

Qy         61 I 61
              |
Db         61 I 61


RESULT 8
US-10-076-604-85
; Sequence 85, Application US/10076604
; Publication No. US20030114372A1
;   GENERAL INFORMATION:
;       APPLICANT: White, Tyler R.
;                  Damm, Deborah
;                  Lesikar, David D.
;                  McFadden, Kathleen
;                  Garrick, Brett L.
;       TITLE OF INVENTION: PROTEASE INHIBITOR PEPTIDES
;       NUMBER OF SEQUENCES: 228
;       CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Foley & Lardner
;             STREET: 3000 K Street, N.W., Suite 500
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20007-5109
;       COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/076,604
;             FILING DATE: 19-Feb-2002
;       PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/09/201,715
;             FILING DATE: 01-Dec-1998
;             APPLICATION NUMBER: US 08/436,555
;             FILING DATE: 08-MAY-1995
;       ATTORNEY/AGENT INFORMATION:
;             NAME: Pelto, Don J.
;             REGISTRATION NUMBER: 33,754
```

```
;           REFERENCE/DOCKET NUMBER: 56324/117
;       TELECOMMUNICATION INFORMATION:
;           TELEPHONE: (202)672-5300
;           TELEFAX: (202)672-5399
;           TELEX: 904136
;   INFORMATION FOR SEQ ID NO: 85:
;       SEQUENCE CHARACTERISTICS:
;           LENGTH: 146 amino acids
;           TYPE: amino acid
;           TOPOLOGY: linear
;       MOLECULE TYPE: protein
;       SEQUENCE DESCRIPTION: SEQ ID NO: 85:
US-10-076-604-85

  Query Match             97.7%;  Score 343;  DB 14;  Length 146;
  Best Local Similarity   98.4%;  Pred. No. 2.8e-34;
  Matches   60;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 EVVREVCSEQAETGPCRAAIYHWYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMAVCGSA 60
              ||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db         86 EVVREVCSEQAETGPCRAAIYRWYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMAVCGSA 145

Qy         61 I 61
              |
Db        146 I 146


RESULT 9
US-10-076-604-216
; Sequence 216, Application US/10076604
; Publication No. US20030114372A1
;   GENERAL INFORMATION:
;       APPLICANT: White, Tyler R.
;                  Damm, Deborah
;                  Lesikar, David D.
;                  McFadden, Kathleen
;                  Garrick, Brett L.
;       TITLE OF INVENTION: PROTEASE INHIBITOR PEPTIDES
;       NUMBER OF SEQUENCES: 228
;       CORRESPONDENCE ADDRESS:
;           ADDRESSEE: Foley & Lardner
;           STREET: 3000 K Street, N.W., Suite 500
;           CITY: Washington
;           STATE: D.C.
;           COUNTRY: USA
;           ZIP: 20007-5109
;       COMPUTER READABLE FORM:
;           MEDIUM TYPE: Floppy disk
;           COMPUTER: IBM PC compatible
;           OPERATING SYSTEM: PC-DOS/MS-DOS
;           SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;           APPLICATION NUMBER: US/10/076,604
;           FILING DATE: 19-Feb-2002
;       PRIOR APPLICATION DATA:
;           APPLICATION NUMBER: US/09/201,715
;           FILING DATE: 01-Dec-1998
;           APPLICATION NUMBER: US 08/436,555
;           FILING DATE: 08-MAY-1995
;       ATTORNEY/AGENT INFORMATION:
;           NAME: Pelto, Don J.
;           REGISTRATION NUMBER: 33,754
;           REFERENCE/DOCKET NUMBER: 56324/117
;       TELECOMMUNICATION INFORMATION:
;           TELEPHONE: (202)672-5300
;           TELEFAX: (202)672-5399
;           TELEX: 904136
;   INFORMATION FOR SEQ ID NO: 216:
;       SEQUENCE CHARACTERISTICS:
;           LENGTH: 61 amino acids
;           TYPE: amino acid
;           STRANDEDNESS: single
;           TOPOLOGY: linear
;       MOLECULE TYPE: protein
;       SEQUENCE DESCRIPTION: SEQ ID NO: 216:
US-10-076-604-216

  Query Match             97.4%;  Score 342;  DB 14;  Length 61;
  Best Local Similarity   96.7%;  Pred. No. 1.5e-34;
  Matches   59;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 EVVREVCSEQAETGPCRAAIYHWYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMAVCGSA 60
              |||||||||||||:||||| ||||||||||||||||||||||||||||||||||||||||
Db          1 EVVREVCSEQAESGPCRALIYHWYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMAVCGSA 60

Qy         61 I 61
              |
Db         61 I 61


RESULT 10
US-10-076-604-223
; Sequence 223, Application US/10076604
; Publication No. US20030114372A1
;   GENERAL INFORMATION:
;       APPLICANT: White, Tyler R.
;                  Damm, Deborah
;                  Lesikar, David D.
;                  McFadden, Kathleen
;                  Garrick, Brett L.
;       TITLE OF INVENTION: PROTEASE INHIBITOR PEPTIDES
;       NUMBER OF SEQUENCES: 228
;       CORRESPONDENCE ADDRESS:
;           ADDRESSEE: Foley & Lardner
;           STREET: 3000 K Street, N.W., Suite 500
;           CITY: Washington
;           STATE: D.C.
;           COUNTRY: USA
;           ZIP: 20007-5109
;       COMPUTER READABLE FORM:
;           MEDIUM TYPE: Floppy disk
;           COMPUTER: IBM PC compatible
;           OPERATING SYSTEM: PC-DOS/MS-DOS
;           SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;           APPLICATION NUMBER: US/10/076,604
;           FILING DATE: 19-Feb-2002
;       PRIOR APPLICATION DATA:
;           APPLICATION NUMBER: US/09/201,715
;           FILING DATE: 01-Dec-1998
;           APPLICATION NUMBER: US 08/436,555
;           FILING DATE: 08-MAY-1995
;       ATTORNEY/AGENT INFORMATION:
;           NAME: Pelto, Don J.
;           REGISTRATION NUMBER: 33,754
;           REFERENCE/DOCKET NUMBER: 56324/117
;       TELECOMMUNICATION INFORMATION:
;           TELEPHONE: (202)672-5300
;           TELEFAX: (202)672-5399
;           TELEX: 904136
;   INFORMATION FOR SEQ ID NO: 223:
;       SEQUENCE CHARACTERISTICS:
;           LENGTH: 61 amino acids
;           TYPE: amino acid
;           STRANDEDNESS: single
;           TOPOLOGY: linear
;       MOLECULE TYPE: protein
;       SEQUENCE DESCRIPTION: SEQ ID NO: 223:
US-10-076-604-223

  Query Match             97.4%;  Score 342;  DB 14;  Length 61;
  Best Local Similarity   96.7%;  Pred. No. 1.5e-34;
  Matches   59;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 EVVREVCSEQAETGPCRAAIYHWYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMAVCGSA 60
              |||||||||||||||||  ||||||||||||||||||||||||||||||||||||||||
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Db          1 EVVREVCSEQAETGPCRGLIYHWYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMAVCGSA 60

Qy         61 I 61
              |
Db         61 I 61


RESULT 11
US-10-076-604-204
; Sequence 204, Application US/10076604
; Publication No. US20030114372A1
;   GENERAL INFORMATION:
;        APPLICANT: White, Tyler R.
;                   Damm, Deborah
;                   Lesikar, David D.
;                   McFadden, Kathleen
;                   Garrick, Brett L.
;        TITLE OF INVENTION: PROTEASE INHIBITOR PEPTIDES
;        NUMBER OF SEQUENCES: 228
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Foley & Lardner
;             STREET: 3000 K Street, N.W., Suite 500
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20007-5109
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/076,604
;             FILING DATE: 19-Feb-2002
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/09/201,715
;             FILING DATE: 01-Dec-1998
;             APPLICATION NUMBER: US 08/436,555
;             FILING DATE: 08-MAY-1995
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Pelto, Don J.
;             REGISTRATION NUMBER: 33,754
;             REFERENCE/DOCKET NUMBER: 56324/117
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (202)672-5300
;             TELEFAX: (202)672-5399
;             TELEX: 904136
;   INFORMATION FOR SEQ ID NO: 204:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 61 amino acids
;             TYPE: amino acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: protein
;        SEQUENCE DESCRIPTION: SEQ ID NO: 204:
US-10-076-604-204

  Query Match             97.2%;  Score 341;  DB 14;  Length 61;
  Best Local Similarity   96.7%;  Pred. No. 2e-34;
  Matches   59;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 EVVREVCSEQAETGPCRAAIYHWYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMAVCGSA 60
              |||||||||||||||||| :|||||||||||||||||||||||||||||||||||||||||
Db          1 EVVREVCSEQAETGPCRALIWHWYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMAVCGSA 60

Qy         61 I 61
              |
Db         61 I 61


RESULT 12
US-10-076-604-215
; Sequence 215, Application US/10076604
; Publication No. US20030114372A1
;   GENERAL INFORMATION:
;        APPLICANT: White, Tyler R.
;                   Damm, Deborah
;                   Lesikar, David D.
;                   McFadden, Kathleen
;                   Garrick, Brett L.
;        TITLE OF INVENTION: PROTEASE INHIBITOR PEPTIDES
;        NUMBER OF SEQUENCES: 228
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Foley & Lardner
;             STREET: 3000 K Street, N.W., Suite 500
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20007-5109
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/076,604
;             FILING DATE: 19-Feb-2002
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/09/201,715
;             FILING DATE: 01-Dec-1998
;             APPLICATION NUMBER: US 08/436,555
;             FILING DATE: 08-MAY-1995
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Pelto, Don J.
;             REGISTRATION NUMBER: 33,754
;             REFERENCE/DOCKET NUMBER: 56324/117
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (202)672-5300
;             TELEFAX: (202)672-5399
;             TELEX: 904136
;   INFORMATION FOR SEQ ID NO: 215:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 61 amino acids
;             TYPE: amino acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: protein
;        SEQUENCE DESCRIPTION: SEQ ID NO: 215:
US-10-076-604-215

  Query Match             97.2%;  Score 341;  DB 14;  Length 61;
  Best Local Similarity   96.7%;  Pred. No. 2e-34;
  Matches   59;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 EVVREVCSEQAETGPCRAAIYHWYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMAVCGSA 60
              |||||||||||| ||||| ||||||||||||||||||||||||||||||||||||||||||
Db          1 EVVREVCSEQAEVGPCRALIYHWYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMAVCGSA 60

Qy         61 I 61
              |
Db         61 I 61


RESULT 13
US-10-076-604-219
; Sequence 219, Application US/10076604
; Publication No. US20030114372A1
;   GENERAL INFORMATION:
;        APPLICANT: White, Tyler R.
;                   Damm, Deborah
;                   Lesikar, David D.
;                   McFadden, Kathleen
;                   Garrick, Brett L.
;        TITLE OF INVENTION: PROTEASE INHIBITOR PEPTIDES
;        NUMBER OF SEQUENCES: 228
;        CORRESPONDENCE ADDRESS:
```

```
;            ADDRESSEE: Foley & Lardner
;            STREET: 3000 K Street, N.W., Suite 500
;            CITY: Washington
;            STATE: D.C.
;            COUNTRY: USA
;            ZIP: 20007-5109
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/10/076,604
;            FILING DATE: 19-Feb-2002
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: US/09/201,715
;            FILING DATE: 01-Dec-1998
;            APPLICATION NUMBER: US 08/436,555
;            FILING DATE: 08-MAY-1995
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Pelto, Don J.
;            REGISTRATION NUMBER: 33,754
;            REFERENCE/DOCKET NUMBER: 56324/117
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: (202)672-5300
;            TELEFAX: (202)672-5399
;            TELEX: 904136
;   INFORMATION FOR SEQ ID NO: 219:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 61 amino acids
;            TYPE: amino acid
;            STRANDEDNESS: single
;            TOPOLOGY: linear
;       MOLECULE TYPE: protein
;       SEQUENCE DESCRIPTION: SEQ ID NO: 219:
US-10-076-604-219

  Query Match             96.9%;  Score 340;  DB 14;  Length 61;
  Best Local Similarity   96.7%;  Pred. No. 2.6e-34;
  Matches   59;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 EVVREVCSEQAETGPCRAAIYHWYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMAVCGSA 60
              ||||||||||||| ||||| ||||||||||||||||||||||||||||||||||||||||
Db          1 EVVREVCSEQAEIGPCRALIYHWYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMAVCGSA 60

Qy         61 I 61
              |
Db         61 I 61


RESULT 14
US-10-076-604-171
; Sequence 171, Application US/10076604
; Publication No. US20030114372A1
;   GENERAL INFORMATION:
;       APPLICANT: White, Tyler R.
;                  Damm, Deborah
;                  Lesikar, David D.
;                  McFadden, Kathleen
;                  Garrick, Brett L.
;       TITLE OF INVENTION: PROTEASE INHIBITOR PEPTIDES
;       NUMBER OF SEQUENCES: 228
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Foley & Lardner
;            STREET: 3000 K Street, N.W., Suite 500
;            CITY: Washington
;            STATE: D.C.
;            COUNTRY: USA
;            ZIP: 20007-5109
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/10/076,604
;            FILING DATE: 19-Feb-2002
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: US/09/201,715
;            FILING DATE: 01-Dec-1998
;            APPLICATION NUMBER: US 08/436,555
;            FILING DATE: 08-MAY-1995
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Pelto, Don J.
;            REGISTRATION NUMBER: 33,754
;            REFERENCE/DOCKET NUMBER: 56324/117
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: (202)672-5300
;            TELEFAX: (202)672-5399
;            TELEX: 904136
;   INFORMATION FOR SEQ ID NO: 171:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 61 amino acids
;            TYPE: amino acid
;            STRANDEDNESS: single
;            TOPOLOGY: linear
;       MOLECULE TYPE: protein
;       SEQUENCE DESCRIPTION: SEQ ID NO: 171:
US-10-076-604-171

  Query Match             96.6%;  Score 339;  DB 14;  Length 61;
  Best Local Similarity   96.7%;  Pred. No. 3.5e-34;
  Matches   59;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 EVVREVCSEQAETGPCRAAIYHWYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMAVCGSA 60
              |||||||||||||||||||: ||||||||||||||||||||||||||||||||||||||||
Db          1 EVVREVCSEQAETGPCRAAIFRWYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMAVCGSA 60

Qy         61 I 61
              |
Db         61 I 61


RESULT 15
US-10-076-604-178
; Sequence 178, Application US/10076604
; Publication No. US20030114372A1
;   GENERAL INFORMATION:
;       APPLICANT: White, Tyler R.
;                  Damm, Deborah
;                  Lesikar, David D.
;                  McFadden, Kathleen
;                  Garrick, Brett L.
;       TITLE OF INVENTION: PROTEASE INHIBITOR PEPTIDES
;       NUMBER OF SEQUENCES: 228
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Foley & Lardner
;            STREET: 3000 K Street, N.W., Suite 500
;            CITY: Washington
;            STATE: D.C.
;            COUNTRY: USA
;            ZIP: 20007-5109
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/10/076,604
;            FILING DATE: 19-Feb-2002
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: US/09/201,715
;            FILING DATE: 01-Dec-1998
;            APPLICATION NUMBER: US 08/436,555
;            FILING DATE: 08-MAY-1995
;       ATTORNEY/AGENT INFORMATION:
```

; NAME: Pelto, Don J.
; REGISTRATION NUMBER: 33,754
; REFERENCE/DOCKET NUMBER: 56324/117
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 178:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 61 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 178:
US-10-076-604-178

Query Match 96.6%; Score 339; DB 14; Length 61;
Best Local Similarity 96.7%; Pred. No. 3.5e-34;
Matches 59; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```
Qy          1 EVVREVCSEQAETGPCRAAIYHWYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMAVCGSA 60
              |||||||||||||||||| || ||||||||||||||||||||||||||||||||||||||
Db          1 EVVREVCSEQAETGPCRAGIYRWYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMAVCGSA 60

Qy         61 I 61
              |
Db         61 I 61
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Search completed: April 8, 2004, 09:31:21
Job time : 40 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: April 8, 2004, 09:31:26 ; Search time 21 Seconds
(without alignments)
279.413 Million cell updates/sec

Title: US-10-076-604-208
Perfect score: 351
Sequence: 1 EVVREVCSEQAETGPCRAAI.....GNRNNFDTEEYCMAVCGSAI 61

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	329	93.7	484	4	A32761	hypothetical Alzhe
2	326	92.9	770	1	QRHUA4	Alzheimer's diseas
3	317	90.3	100	2	A32282	Alzheimer's diseas
4	304	86.6	76	2	S06678	Alzheimer's diseas
5	303	86.3	76	2	S03607	Alzheimer's diseas
6	299	85.2	76	2	S04855	Alzheimer's diseas
7	288	82.1	747	2	JH0773	Alzheimer's diseas
8	238	67.8	751	2	A49974	beta-amyloid precu
9	238	67.8	763	2	A49321	amyloid beta (A4)
10	238	67.8	765	2	S42880	amyloid precursor-
11	236	67.2	111	2	S41082	amyloid precursor
12	168	47.9	55	2	S30332	proteinase inhibit
13	161	45.9	252	2	JG0185	hepatocyte growth
14	160	45.6	2225	2	T26063	hypothetical prote
15	158	45.0	58	1	TIHABK	isoinhibitor K (BP
16	157	44.7	1558	2	C89114	protein C37C3.6a [
17	157	44.7	2167	2	T34395	hypothetical prote
18	155	44.2	3137	2	A37797	collagen alpha 3(V
19	154	43.9	58	2	S10063	isoaprotinin G2 -
20	153	43.6	67	1	TIBOC	trypsin inhibitor,
21	153	43.6	100	1	TIBO	basic proteinase i
22	153	43.6	302	1	TIRTGK	tissue factor path
23	151	43.0	1965	2	T33216	hypothetical prote
24	150	42.7	60	1	TIVRV2	venom basic protei
25	150	42.7	123	2	A29652	inter-alpha-trypsi
26	148	42.2	59	2	S00371	isoaprotinin G1 -
27	148	42.2	352	1	TIBOBI	alpha-1-microglobu
28	147	41.9	337	1	TIPGBI	alpha-1-microglobu
29	147	41.9	349	2	S35708	alpha-1-microglobu
30	146	41.6	62	2	S07451	proteinase inhibit
31	146	41.6	3176	2	CGHU3A	collagen alpha 3(V
32	145	41.3	64	2	S41399	Kunitz-type protei
33	144	41.0	60	1	TIBOR	serum basic protei
34	143	40.7	349	2	S21089	alpha-1-microglobu
35	143	40.7	352	1	HCHU	alpha-1-microglobu
36	142	40.5	100	1	TIBOSP	spleen basic prote
37	142	40.5	125	1	TIHOBI	alpha-1-microglobu
38	142	40.5	304	1	JC2264	tissue factor path
39	142	40.5	1743	2	T26859	hypothetical prote
40	140	39.9	249	2	T32060	hypothetical prote
41	139	39.6	396	2	S53325	tissue factor path
42	138	39.3	61	1	TIVIT1	venom basic protei
43	138	39.3	304	1	TIHUGK	tissue factor path
44	137	39.0	2150	2	T32497	hypothetical prote
45	136	38.7	110	1	TITTOR	basic proteinase i

ALIGNMENTS

RESULT 1
A32761
hypothetical Alzheimer's disease amyloid beta protein, Alu-containing clone - human (fr
C;Species: Homo sapiens (man)
C;Date: 29-Jan-1990 #sequence_revision 10-Apr-1996 #text_change 10-Apr-1996
C;Accession: A32761
R;de Sauvage, F.; Octave, J.N.
Science 245, 651-653, 1989
A;Title: A novel mRNA of the A4 amyloid precursor gene coding for a possibly secreted p
A;Reference number: A32761; MUID:89346754; PMID:2569763
A;Accession: A32761
A;Molecule type: mRNA
A;Residues: 1-484 <DES>
A;Cross-references: GB:M28373
A;Note: the authors translated the codon ATG for residue 433 as Leu
C;Comment: This is the hypothetical translation of a sequence believed to contain cloni
C;Keywords: cloning artifact

Query Match 93.7%; Score 329; DB 4; Length 484;
Best Local Similarity 95.1%; Pred. No. 1.7e-30;
Matches 58; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```
Qy          1 EVVREVCSEQAETGPCRAAIYHWYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMAVCGSA 60
              ||||||||||||||||||  |  ||||||||||||||||||||||||||||||||||||
Db        206 EVVREVCSEQAETGPCRAMISRWYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMAVCGSA 265

Qy         61 I 61
              |
Db        266 I 266
```

RESULT 2
QRHUA4
Alzheimer's disease amyloid beta protein precursor [validated] - human
N;Alternate names: Alzheimer's disease amyloid A4 protein; coagulation factor XIa inhib
N;Contains: amyloid beta protein long, plaque form; amyloid beta protein short, vascula
protein precursor splice form APP(770)
C;Species: Homo sapiens (man)
C;Date: 30-Jun-1987 #sequence_revision 28-Jul-1995 #text_change 15-Sep-2000
C;Accession: S02260; S05194; A32277; A33260; A35486; I39452; I39451; I39453; I59562; A4
4668; A28583; A29302; A60805; JL0038; S06121; A60355; A59011; A38384; S29076; S38252; S
R;Lemaire, H.G.; Salbaum, J.M.; Multhaup, G.; Kang, J.; Bayney, R.M.; Unterbeck, A.; Be
Nucleic Acids Res. 17, 517-522, 1989
A;Title: The PreA4(695) precursor protein of Alzheimer's disease A4 amyloid is encoded
A;Reference number: S02260; MUID:89128427; PMID:2783775
A;Accession: S02260
A;Molecule type: DNA
A;Residues: 1-288,'V',365-770 <LEM1>
A;Cross-references: EMBL:X13466
A;Note: alternative splice form APP(695)
R;Lemaire, H.G.
submitted to the EMBL Data Library, November 1988

A;Reference number: S05194
A;Accession: S05194
A;Molecule type: DNA
A;Residues: 1-14,'VW',17-288,'V',365-770 <LEM2>
A;Cross-references: EMBL:X13466; NID:g35598; PIDN:CAA31830.1; PID:g871360
A;Note: alternative splice form APP(695)
R;La Fauci, G.; Lahiri, D.K.; Salton, S.R.J.; Robakis, N.K.
Biochem. Biophys. Res. Commun. 159, 297-304, 1989
A;Title: Characterization of the 5'-end region and the first two exons of the beta-prote
A;Reference number: A32277; MUID:89165870; PMID:2538123
A;Accession: A32277
A;Molecule type: DNA
A;Residues: 1-75 <LAF>
A;Cross-references: GB:M24546; GB:M24547; NID:g341202; PIDN:AAC13654.1; PID:g516074
R;Johnstone, E.M.; Chaney, M.O.; Moore, R.E.; Ward, K.E.; Norris, F.H.; Little, S.P.
Biochem. Biophys. Res. Commun. 163, 1248-1255, 1989
A;Title: Alzheimer's disease amyloid peptide is encoded by two exons and shows similarit
A;Reference number: A33260; MUID:89392030; PMID:2675837
A;Accession: A33260
A;Molecule type: DNA
A;Residues: 656-737 <JOH>
A;Cross-references: GB:M29270; NID:g178863; PIDN:AAA51768.1; PID:g178865
R;Prelli, F.; Levy, E.; van Duinen, S.G.; Bots, G.T.A.M.; Luyendijk, W.; Frangione, B.
Biochem. Biophys. Res. Commun. 170, 301-307, 1990
A;Title: Expression of a normal and variant Alzheimer's beta-protein gene in amyloid of
A;Reference number: A35486; MUID:90321244; PMID:2196878
A;Accession: A35486
A;Molecule type: DNA
A;Residues: 672-710 <PRE1>
A;Note: 693-Gln was found in DNA isolated from HCHWA-D patients
R;Yoshikai, S.I.; Sasaki, H.; Doh-ura, K.; Furuya, H.; Sakaki, Y.
Gene 87, 257-263, 1990
A;Title: Genomic organization of the human amyloid beta-protein precursor gene.
A;Reference number: I39451; MUID:90236318; PMID:2110105
A;Accession: I39452
A;Status: nucleic acid sequence not shown; translation not shown; translated from GB/EME
A;Molecule type: DNA
A;Residues: 1-770 <YOS1>
A;Cross-references: GB:M33112; NID:g178613; PIDN:AAB59502.1; PID:g178616
A;Accession: I39451
A;Status: nucleic acid sequence not shown; translation not shown; translated from GB/EME
A;Molecule type: DNA
A;Residues: 1-530,'QWLMPVIPAFWEAKVGR' <YOS2>
A;Cross-references: GB:M34875; NID:g178608; PIDN:AAB59501.1; PID:g178615
R;Yoshikai, S.I.; Sasaki, H.; Doh-ura, K.; Furuya, H.; Sakaki, Y.
Gene 102, 291-292, 1991
A;Reference number: A59020; MUID:91340168; PMID:1908403
A;Contents: annotation; erratum
A;Note: revised physical map for reference I39451
R;Levy, E.; Carman, M.D.; Fernandez-Madrid, I.J.; Power, M.D.; Lieberburg, I.; van Duine
Science 248, 1124-1126, 1990
A;Title: Mutation of the Alzheimer's disease amyloid gene in hereditary cerebral hemorrh
A;Reference number: I39453; MUID:90260663; PMID:2111584
A;Accession: I39453
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 656-737 <LEV>
A;Cross-references: GB:M37896; NID:g178618; PIDN:AAA51727.1; PID:g178620
A;Note: a mutation with 693-Gln is presented
R;Murrell, J.; Farlow, M.; Ghetti, B.; Benson, M.D.
Science 254, 97-99, 1991
A;Title: A mutation in the amyloid precursor protein associated with hereditary Alzheime
A;Reference number: I59562; MUID:92022553; PMID:1925564
A;Accession: I59562
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 689-716,'F',718-737 <MUR>
A;Cross-references: GB:S57665; NID:g236720; PIDN:AAB19991.1; PID:g236721
R;Kamino, K.; Orr, H.T.; Payami, H.; Wijsman, E.M.; Alonso, M.E.; Pulst, S.M.; Anderson,
arakis, S.E.; Korenberg, J.R.; Sharma, V.; Kukull, W.; Larson, E.; Heston, L.L.; Martin,
Am. J. Hum. Genet. 51, 998-1014, 1992
A;Title: Linkage and mutational analysis of familial Alzheimer disease kindreds for the
A;Reference number: A44017; MUID:93035397; PMID:1415269

A;Accession: A44017
A;Molecule type: DNA
A;Residues: 687-692,'G',694-718 <KAM1>
A;Cross-references: GB:S45135; NID:g257377; PIDN:AAB23645.1; PID:g257378
A;Experimental source: familial Alzheimer disease family SB
A;Note: sequence extracted from NCBI backbone (NCBIP:115374)
A;Accession: B44017
A;Molecule type: DNA
A;Residues: 687-718 <KAM2>
A;Cross-references: GB:S45136; NID:g257379; PIDN:AAB23646.1; PID:g257380
A;Experimental source: familial Alzheimer disease family LIT
A;Note: sequence extracted from NCBI backbone (NCBIP:115376)
A;Note: this sequence has a silent mutation
R;Kang, J.; Lemaire, H.G.; Unterbeck, A.; Salbaum, J.M.; Masters, C.L.; Grzeschik, K.H
Nature 325, 733-736, 1987
A;Title: The precursor of Alzheimer's disease amyloid A4 protein resembles a cell-surf.
A;Reference number: A03134; MUID:87144572; PMID:2881207
A;Accession: A03134
A;Molecule type: mRNA
A;Residues: 1-288,'V',365-770 <KAN>
A;Cross-references: GB:Y00264; NID:g28525; PIDN:CAA68374.1; PID:g28526
A;Note: alternative splice form APP(695)
R;Robakis, N.K.; Ramakrishna, N.; Wolfe, G.; Wisniewski, H.M.
Proc. Natl. Acad. Sci. U.S.A. 84, 4190-4194, 1987
A;Title: Molecular cloning and characterization of a cDNA encoding the cerebrovascular
A;Reference number: A29030; MUID:87231971; PMID:3035574
A;Accession: A29030
A;Molecule type: mRNA
A;Residues: 284-288,'V',365-646,'E',648-770 <ROB>
A;Cross-references: GB:M16765; NID:g178539; PIDN:AAA51722.1; PID:g178540
A;Note: the authors translated the codon GAG for residue 647 as Asp
R;Goldgaber, D.; Lerman, M.I.; McBride, O.W.; Saffiotti, U.; Gajdusek, D.C.
Science 235, 877-880, 1987
A;Title: Characterization and chromosomal localization of a cDNA encoding brain amyloi
A;Reference number: A47584; MUID:87120328; PMID:3810169
A;Accession: A47584
A;Molecule type: mRNA
A;Residues: 674-756,'S',758-770 <GOL>
A;Cross-references: GB:M15533; NID:g178706; PIDN:AAA35540.1; PID:g178707
A;Experimental source: brain
R;Tanzi, R.E.; Gusella, J.F.; Watkins, P.C.; Bruns, G.A.P.; St George-Hyslop, P.; Van
Science 235, 880-884, 1987
A;Title: Amyloid beta protein gene: cDNA, mRNA distribution, and genetic linkage near t
A;Reference number: A47585; MUID:87120329; PMID:2949367
A;Accession: A47585
A;Molecule type: mRNA
A;Residues: 674-703 <TAN1>
A;Cross-references: GB:M15532; NID:g177957; PIDN:AAA51564.1; PID:g177958
R;Dyrks, T.; Weidemann, A.; Multhaup, G.; Salbaum, J.M.; Lemaire, H.G.; Kang, J.; Muell
EMBO J. 7, 949-957, 1988
A;Title: Identification, transmembrane orientation and biogenesis of the amyloid A4 pre
A;Reference number: S02638; MUID:88296437; PMID:2900137
A;Accession: S02638
A;Molecule type: mRNA
A;Residues: 672-678 <DYR>
R;Tanzi, R.E.; McClatchey, A.I.; Lamperti, E.D.; Villa-Komaroff, L.; Gusella, J.F.; Nev
Nature 331, 528-530, 1988
A;Title: Protease inhibitor domain encoded by an amyloid protein precursor mRNA associa
A;Reference number: S00707; MUID:88122640; PMID:2893290
A;Accession: S00707
A;Molecule type: mRNA
A;Residues: 286-344,'I',365-366 <TAN2>
A;Cross-references: EMBL:X06982; NID:g28817; PIDN:CAA30042.1; PID:g929612
A;Experimental source: promyelocytic leukemia cell line HL60
A;Note: alternative splice form APP(751)
R;Ponte, P.; Gonzalez-DeWhitt, P.; Schilling, J.; Miller, J.; Hsu, D.; Greenberg, B.; I
Nature 331, 525-527, 1988
A;Title: A new A4 amyloid mRNA contains a domain homologous to serine proteinase inhibi
A;Reference number: S00925; MUID:88122639; PMID:2893289
A;Accession: S00925
A;Molecule type: mRNA
A;Residues: 1-344,'I',365-770 <PO2>
A;Cross-references: GB:X06989; EMBL:Y00297; NID:g28720; PIDN:CAA30050.1; PID:g28721

```
A;Note: alternative splice form APP(751)
R;Kitaguchi, N.; Takahashi, Y.; Tokushima, Y.; Shiojiri, S.; Ito, H.
Nature 331, 530-532, 1988
A;Title: Novel precursor of Alzheimer's disease amyloid protein shows protease inhibitor
A;Reference number: A38949; MUID:88122641; PMID:2893291
A;Accession: A38949
A;Molecule type: mRNA
A;Residues: 287-367 <KIT>
A;Cross-references: GB:X06981; NID:g28816; PIDN:CAA30041.1; PID:g929611
A;Experimental source: glioblastoma cell line
A;Note: alternative splice form APP(770)
R;Vitek, M.P.; Rascol, C.G.; de Sauvage, F.; Vitek, S.M.; Bartus, R.T.; Beer, B.; Ashton
Brain Res. Mol. Brain Res. 4, 121-131, 1988
A;Title: Absence of mutation in the beta-amyloid cDNAs cloned from the brains of three p
A;Reference number: A30320
A;Accession: A30320
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 284-288,'V',365-770 <VIT1>
A;Accession: B30320
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 122-288,'V',365-770 <VIT2>
A;Accession: C30320
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 606-770 <VIT3>
R;Zain, S.B.; Salim, M.; Chou, W.G.; Sajdel-Sulkowska, E.M.; Majocha, R.E.; Marotta, C.A
Proc. Natl. Acad. Sci. U.S.A. 85, 929-933, 1988
A;Title: Molecular cloning of amyloid cDNA derived from mRNA of the Alzheimer disease br
A;Reference number: A31087; MUID:88124954; PMID:2893379
A;Accession: A31087
A;Molecule type: mRNA
A;Residues: 507-770 <ZAI>
A;Cross-references: GB:M18734; NID:g178572; PIDN:AAA51726.1; PID:g178573
A;Note: the authors translated the codon GAA for residue 599 as Gly, ACC for residue 603
8 as Val, GTG for residue 609 as Asn, AAT for residue 610 as Gly, and GGT for residue 65
A;Note: the cited Genbank accession number, J03594, is not in release 101.0
R;Masters, C.L.; Multhaup, G.; Simms, G.; Pottgiesser, J.; Martins, R.N.; Beyreuther, K.

  Query Match             92.9%;  Score 326;  DB 1;  Length 770;
  Best Local Similarity   93.4%;  Pred. No. 5.7e-30;
  Matches   57;  Conservative    1;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 EVVREVCSEQAETGPCRAAIYHWYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMAVCGSA 60
              |||||||||||||||||| |  ||||||||||||||||||||||||||||||||||||
Db        285 EVVREVCSEQAETGPCRAMISRWYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMAVCGSA 344

Qy         61 I 61
              :
Db        345 M 345


RESULT 3
A32282
Alzheimer's disease amyloid beta protein precursor - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 17-Aug-1989 #sequence_revision 17-Aug-1989 #text_change 13-Aug-1999
C;Accession: A32282
R;Yamada, T.; Sasaki, H.; Dohura, K.; Goto, I.; Sakaki, Y.
Biochem. Biophys. Res. Commun. 158, 906-912, 1989
A;Title: Structure and expression of the alternatively-spliced forms of mRNA for the mou
A;Reference number: A32282; MUID:89149813; PMID:2493250
A;Accession: A32282
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-100 <YAM>
A;Cross-references: GB:M24397; NID:g200350; PIDN:AAA39929.1; PID:g200351
C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase i
C;Keywords: alternative splicing
F;11-61/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>

  Query Match             90.3%;  Score 317;  DB 2;  Length 100;
  Best Local Similarity   93.2%;  Pred. No. 9.9e-30;
  Matches   55;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 EVVREVCSEQAETGPCRAAIYHWYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMAVCGS 59
              |||||||||||||||||| |  |||||||||| ||||||||||||||||||||||||||
Db          5 EVVREVCSEQAETGPCRAMISRWYFDVTEGKCVPFFYGGCGGNRNNFDTEEYCMAVCGS 63


RESULT 4
S06678
Alzheimer's disease amyloid beta protein - rhesus macaque (fragment)
C;Species: Macaca mulatta (rhesus macaque)
C;Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 13-Aug-1999
C;Accession: S06678
R;Koo, E.H.; Sisodia, S.S.; Price, D.L.
submitted to the EMBL Data Library, July 1989
A;Reference number: S06678
A;Accession: S06678
A;Molecule type: mRNA
A;Residues: 1-76 <KOO>
A;Cross-references: EMBL:X15985; NID:g38080; PIDN:CAA34116.1; PID:g930135
C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase
C;Keywords: alternative splicing; serine proteinase inhibitor
F;3-53/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>

  Query Match             86.6%;  Score 304;  DB 2;  Length 76;
  Best Local Similarity   91.2%;  Pred. No. 2.5e-28;
  Matches   52;  Conservative    1;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          5 EVCSEQAETGPCRAAIYHWYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMAVCGSAI 61
              | ||||||||||||||| |  |||||||||||||||||||||||||||||||||| :
Db          1 EVCSEQAETGPCRAMISRWYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMAVCGSVM 57


RESULT 5
S03607
Alzheimer's disease amyloid A4 protein - rat (fragment)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 13-Aug-1999
C;Accession: S03607
R;Kang, J.; Mueller-Hill, B.
Nucleic Acids Res. 17, 2130, 1989
A;Title: The sequence of the two extra exons in rat preA4.
A;Reference number: S03607; MUID:89183625; PMID:2648331
A;Accession: S03607
A;Molecule type: mRNA
A;Residues: 1-76 <KAN>
A;Cross-references: EMBL:X14066; NID:g56957; PIDN:CAA32229.1; PID:g930262
C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase
C;Keywords: alternative splicing; serine proteinase inhibitor; transmembrane protein
F;3-53/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>

  Query Match             86.3%;  Score 303;  DB 2;  Length 76;
  Best Local Similarity   94.5%;  Pred. No. 3.2e-28;
  Matches   52;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          5 EVCSEQAETGPCRAAIYHWYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMAVCGS 59
              |||||||||||||| |  ||||||||||||||||||||||||||||||||||||
Db          1 EVCSEQAETGPCRAMISRWYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMAVCGS 55


RESULT 6
S04855
Alzheimer's disease amyloid A4 protein - mouse (fragment)
C;Species: Mus musculus domesticus (western European house mouse)
C;Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 13-Aug-1999
C;Accession: S04855
R;Fukuchi, K.I.; Martin, G.M.; Deeb, S.S.
Nucleic Acids Res. 17, 5396, 1989
A;Title: Sequence of the protease inhibitor domain of the A4 amyloid protein precursor
A;Reference number: S04855; MUID:89345111; PMID:2569710
A;Accession: S04855
A;Molecule type: mRNA
```

```
A;Residues: 1-76 <FUK>
A;Cross-references: EMBL:X15210; NID:g49965; PIDN:CAA33280.1; PID:g930133
A;Note: the authors translated the codon GAT for residue 74 as Val
C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase i
C;Keywords: alternative splicing; serine proteinase inhibitor; transmembrane protein
F;3-53/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>

  Query Match             85.2%;  Score 299;  DB 2;  Length 76;
  Best Local Similarity   92.7%;  Pred. No. 9.4e-28;
  Matches   51;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          5 EVCSEQAETGPCRAAIYHWYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMAVCGS 59
              ||||||||||||||| |  |||||||||| ||||||||||||||||||||||||||
Db          1 EVCSEQAETGPCRAMISRWYFDVTEGKCVPFFYGGCGGNRNNFDTEEYCMAVCGS 55


RESULT 7
JH0773
Alzheimer's disease amyloid beta protein precursor - African clawed frog
C;Species: Xenopus laevis (African clawed frog)
C;Date: 10-Jun-1993 #sequence_revision 10-Jun-1993 #text_change 13-Aug-1999
C;Accession: JH0773
R;Okado, H.; Okamoto, H.
Biochem. Biophys. Res. Commun. 189, 1561-1568, 1992
A;Title: A Xenopus homologue of the human beta-amyloid precursor protein: developmental
A;Reference number: JH0773; MUID:93129227; PMID:1282805
A;Accession: JH0773
A;Molecule type: mRNA
A;Residues: 1-747 <OKA>
A;Cross-references: GB:S52417; NID:g263150; PIDN:AAB24853.1; PID:g263151
A;Experimental source: larva
C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase i
C;Keywords: alternative splicing; amyloid
F;287-337/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>

  Query Match             82.1%;  Score 288;  DB 2;  Length 747;
  Best Local Similarity   80.3%;  Pred. No. 1.4e-25;
  Matches   49;  Conservative    5;  Mismatches    7;  Indels    0;  Gaps    0;

Qy          1 EVVREVCSEQAETGPCRAAIYHWYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMAVCGSA 60
              |||||||||||||||||| |  ||:|||| ||| | ||||||||||:::|||||||
Db        281 EVVREVCSEQAETGPCRAMISRWYYDVTESKCAQFIYGGCGGNRNNFESDDYCMAVCGSV 340

Qy         61 I 61
              |
Db        341 I 341


RESULT 8
A49974
beta-amyloid precursor protein 2 homolog APLP2 - mouse
C;Species: Mus musculus (house mouse)
C;Date: 06-Oct-1994 #sequence_revision 18-Nov-1994 #text_change 13-Aug-1999
C;Accession: A49974
R;Slunt, H.H.; Thinakaran, G.; Von Koch, C.; Lo, A.C.; Tanzi, R.E.; Sisodia, S.S.
J. Biol. Chem. 269, 2637-2644, 1994
A;Title: Expression of a ubiquitous, cross-reactive homologue of the mouse beta-amyloid
A;Reference number: A49974; MUID:94132029; PMID:8300594
A;Accession: A49974
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: nucleic acid
A;Residues: 1-751 <SLU>
A;Cross-references: GB:U15571; NID:g558467; PIDN:AAA50603.1; PID:g558468
A;Note: sequence extracted from NCBI backbone (NCBIP:144636)
C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase i
F;310-360/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>

  Query Match             67.8%;  Score 238;  DB 2;  Length 751;
  Best Local Similarity   64.4%;  Pred. No. 8.8e-20;
  Matches   38;  Conservative   11;  Mismatches   10;  Indels    0;  Gaps    0;

Qy          3 VREVCSEQAETGPCRAAIYHWYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMAVCGSAI 61
              |: |||::| |||||| :  ||||:::|||  | ||||||||||::|:|||||| : |
Db        306 VKAVCSQEAMTGPCRAVMPRWYFDLSKGKCVRFIYGGCGGNRNNFESEDYCMAVCKAMI 364


RESULT 9
A49321
amyloid beta (A4) homolog 2 precursor - human
N;Alternate names: CDEI-binding protein
C;Species: Homo sapiens (man)
C;Date: 24-Feb-1994 #sequence_revision 18-Nov-1994 #text_change 13-Aug-1999
C;Accession: A49321; S34644; S40519
R;Sprecher, C.A.; Grant, F.J.; Grimm, G.; O'Hara, P.J.; Norris, F.; Norris, K.; Foster
Biochemistry 32, 4481-4486, 1993
A;Title: Molecular cloning of the cDNA for a human amyloid precursor protein homolog:
A;Reference number: A49321; MUID:93250009; PMID:8485127
A;Accession: A49321
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-763 <SPR>
A;Cross-references: GB:S60099; NID:g300168; PIDN:AAC60589.1; PID:g300169
A;Experimental source: placenta
A;Note: sequence extracted from NCBI backbone (NCBIN:131198, NCBIP:131199)
A;Note: expression was shown in placenta, brain, heart, lung, liver, and kidney
R;von der Kammer, H.; Klaudiny, J.; Hanes, J.; Scheit, K.H.
submitted to the EMBL Data Library, April 1993
A;Description: The human homologue of the murine CDEI binding protein is an amyloid pr
A;Reference number: S34644
A;Accession: S34644
A;Molecule type: mRNA
A;Residues: 1-763 <VON>
A;Cross-references: EMBL:Z22572; NID:g394763; PIDN:CAA80295.1; PID:g394764
R;Wasco, W.; Gurubhagavatula, S.; Paradis, M.; Romano, D.M.; Sisodia, S.S.; Hyman, B.T
Nature Genet. 5, 95-99, 1993
A;Title: Isolation and characterization of APLP2 encoding a homologue of the Alzheimer
A;Reference number: S40519; MUID:94035131; PMID:8220435
A;Accession: S40519
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-763 <WAS>
A;Cross-references: GB:L27631; NID:g450391; PIDN:AAC41701.1; PID:g450392
C;Genetics:
A;Gene: GDB:APLP2; APPL2
A;Cross-references: GDB:139159; OMIM:104776
A;Map position: 11q23-11q25
C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase
C;Keywords: alternative splicing; transmembrane protein
F;310-360/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>

  Query Match             67.8%;  Score 238;  DB 2;  Length 763;
  Best Local Similarity   64.4%;  Pred. No. 8.9e-20;
  Matches   38;  Conservative   11;  Mismatches   10;  Indels    0;  Gaps    0;

Qy          3 VREVCSEQAETGPCRAAIYHWYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMAVCGSAI 61
              |: |||::| |||||| :  ||||:::|||  | ||||||||||::|:|||||| : |
Db        306 VKAVCSQEAMTGPCRAVMPRWYFDLSKGKCVRFIYGGCGGNRNNFESEDYCMAVCKAMI 364


RESULT 10
S42880
amyloid precursor-like protein - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 17-Mar-1999
C;Accession: S42880; S47528
R;Sandbrink, R.; Masters, C.L.; Beyreuther, K.
submitted to the EMBL Data Library, March 1994
A;Description: Complete nucloetide ad deduced amino acid sequence of rat amyloid precu
A;Reference number: S42880
A;Accession: S42880
A;Molecule type: mRNA
A;Residues: 1-765 <SAN>
A;Cross-references: EMBL:X77934
R;Sandbrink, R.; Masters, C.L.; Beyreuther, K.
Biochim. Biophys. Acta 1219, 167-170, 1994
A;Title: Complete nucleotide and deduced amino acid sequence of rat amyloid protein pr
```

```
A;Reference number: S47528; MUID:94368849; PMID:8086458
A;Accession: S47528
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-765 <SA2>
A;Cross-references: EMBL:X77934
C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase i
C;Keywords: alternative splicing
F;312-362/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>

  Query Match             67.8%;  Score 238;  DB 2;  Length 765;
  Best Local Similarity   64.4%;  Pred. No. 8.9e-20;
  Matches   38;  Conservative   11;  Mismatches   10;  Indels    0;  Gaps    0;

Qy          3 VREVCSEQAETGPCRAAIYHWYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMAVCGSAI 61
              |: |||::| |||||| :  ||||:::|||  | ||||||||||||::|:|||||| : |
Db        308 VKAVCSQEAMTGPCRAVMPRWYFDLSKGKCVRFIYGGCGGNRNNFESEDYCMAVCKTMI 366


RESULT 11
S41082
amyloid precursor protein homolog - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 25-Dec-1994 #sequence_revision 03-Aug-1995 #text_change 29-Aug-1997
C;Accession: S41082
R;Petersen, L.C.; Bjorn, S.E.; Norris, F.; Norris, K.; Sprecher, C.; Foster, D.C.
FEBS Lett. 338, 53-57, 1994
A;Title: Expression, purification and characterization of a Kunitz-type protease inhibit
A;Reference number: S41082; MUID:94139895; PMID:8307156
A;Accession: S41082
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-111 <PET>
C;Superfamily: animal Kunitz-type proteinase inhibitor homology
F;59-109/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>

  Query Match             67.2%;  Score 236;  DB 2;  Length 111;
  Best Local Similarity   67.3%;  Pred. No. 2.6e-20;
  Matches   37;  Conservative   10;  Mismatches    8;  Indels    0;  Gaps    0;

Qy          3 VREVCSEQAETGPCRAAIYHWYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMAVC 57
              |: |||::| |||||| :  ||||:::|||  | ||||||||||||::|:|||||
Db         55 VKAVCSQEAMTGPCRAVMPRWYFDLSKGKCVRFIYGGCGGNRNNFESEDYCMAVC 109


RESULT 12
S30332
proteinase inhibitor (Kunitz-type) - sea anemone (Stichodactyla helianthus)
C;Species: Stichodactyla helianthus, Stoichactis helianthus (Caribbean sea anemone)
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 16-Jul-1999
C;Accession: S30332
R;Antuch, W.; Berndt, K.D.; Chavez, M.A.; Delfin, J.; Wuethrich, K.
Eur. J. Biochem. 212, 675-684, 1993
A;Title: The NMR solution structure of a Kunitz-type proteinase inhibitor from the sea a
A;Reference number: S30332; MUID:93215644; PMID:8462542
A;Accession: S30332
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-55 <ANT>
C;Superfamily: basic proteinase inhibitor; animal Kunitz-type proteinase inhibitor homol
F;3-53/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>

  Query Match             47.9%;  Score 168;  DB 2;  Length 55;
  Best Local Similarity   51.9%;  Pred. No. 1.1e-12;
  Matches   27;  Conservative    6;  Mismatches   19;  Indels    0;  Gaps    0;

Qy          6 VCSEQAETGPCRAAIYHWYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMAVC 57
              :|||  : | |:     :|||   ||| || |||||| |||:|   | |:|
Db          2 ICSEPKKVGRCKGYFPRFYFDSETGKCTPFIYGGCGGNGNNFETLHQCRAIC 53


RESULT 13
JG0185
hepatocyte growth factor activator inhibitor type 2 - mouse
C;Species: Mus musculus (house mouse)
C;Date: 23-Jul-1999 #sequence_revision 23-Jul-1999 #text_change 11-May-2000
C;Accession: JG0185
R;Itoh, H.; Kataoka, H.; Hamasuna, R.; Kitamura, N.; Koono, M.
Biochem. Biophys. Res. Commun. 255, 740-748, 1999
A;Title: Hepatocyte growth factor activator inhibitor type 2 lacking the first kunitz-
A;Reference number: JG0185; MUID:99160423; PMID:10049781
A;Accession: JG0185
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-252 <ITO>
A;Cross-references: GB:AF099016
C;Superfamily: animal Kunitz-type proteinase inhibitor homology
F;133-183/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>

  Query Match             45.9%;  Score 161;  DB 2;  Length 252;
  Best Local Similarity   45.5%;  Pred. No. 2.7e-11;
  Matches   25;  Conservative   10;  Mismatches   20;  Indels    0;  Gaps    0;

Qy          3 VREVCSEQAETGPCRAAIYHWYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMAVC 57
              | | |      | |||:|  |::::|:| | || |||| || ||: ::| |:  |
Db         34 VHESCGVSKVVGKCRASIPRWWYNITDGSCQPFVYGGCEGNGNNYQSKEECLDKC 88


RESULT 14
T26063
hypothetical protein W01F3.3 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T26063
R;Cummings, P.
submitted to the EMBL Data Library, March 1997
A;Reference number: Z20145
A;Accession: T26063
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-2225 <WIL>
A;Cross-references: EMBL:Z92815; PIDN:CAB07294.1; GSPDB:GN00023; CESP:W01F3.3
A;Experimental source: clone W01F3
C;Genetics:
A;Gene: CESP:W01F3.3
A;Map position: 5
A;Introns: 33/1; 56/1; 100/1; 142/3; 271/3; 451/1; 525/3; 774/1; 1093/1; 1178/1; 1221/

  Query Match             45.6%;  Score 160;  DB 2;  Length 2225;
  Best Local Similarity   47.3%;  Pred. No. 2.6e-10;
  Matches   26;  Conservative    8;  Mismatches   21;  Indels    0;  Gaps    0;

Qy          3 VREVCSEQAETGPCRAAIYHWYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMAVC 57
              : | | :  | |||:      |||:| :| | || |||| ||||:|  |:: |   |
Db       1119 IEEKCLQPVEPGPCKNFADRWYFNVDDGTCHPFKYGGCAGNRNHFFTQKECEVHC 1173


RESULT 15
TIHABK
isoinhibitor K (BPI type) - Roman snail
C;Species: Helix pomatia (Roman snail)
C;Date: 23-Oct-1981 #sequence_revision 23-Oct-1981 #text_change 05-Aug-1994
C;Accession: A91232; A01225
R;Tschesche, H.; Dietl, T.
Eur. J. Biochem. 58, 439-451, 1975
A;Title: The amino-acid sequence of isoinhibitor K from snails (Helix pomatia). A seque
A;Reference number: A91232; MUID:76043680; PMID:1183446
A;Accession: A91232
A;Molecule type: protein
A;Residues: 1-58 <TSC>
R;Dietl, T.; Tschesche, H.
Hoppe-Seyler's Z. Physiol. Chem. 357, 139-145, 1976
A;Title: Die Disulfidbruecken des Trypsin-Kallikrein-Inhibitors K aus Weinbergschnecker
A;Reference number: A91666; MUID:76141310; PMID:3462
A;Contents: annotation; disulfide bonds
C;Comment: This is one of several isoinhibitors of broad specificity that are secreted
```

C;Superfamily: basic proteinase inhibitor; animal Kunitz-type proteinase inhibitor homol
C;Keywords: pyroglutamic acid; serine proteinase inhibitor
F;7-57/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F;7-57,16-40,32-53/Disulfide bonds: #status predicted

Query Match 45.0%; Score 158; DB 1; Length 58;
Best Local Similarity 49.0%; Pred. No. 1.6e-11;
Matches 25; Conservative 8; Mismatches 18; Indels 0; Gaps 0;

```
Qy          7 CSEQAETGPCRAAIYHWYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMAVC 57
              |:  ||||||:|:   :|::   | |  | |||| ||:| ||| : |   ||
Db          7 CNLPAETGPCKASFRQYYYNSKSGGCQQFIYGGCRGNQNRFDTTQQCQGVC 57
```

Search completed: April 8, 2004, 09:34:46
Job time : 22 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: April 8, 2004, 09:26:36 ; Search time 11 Seconds
(without alignments)
288.753 Million cell updates/sec

Title: US-10-076-604-208
Perfect score: 351
Sequence: 1 EVVREVCSEQAETGPCRAAI.....GNRNNFDTEEYCMAVCGSAI 61

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	326	92.9	770	1	A4_HUMAN	P05067 h amyloid b
2	325	92.6	751	1	A4_SAISC	Q95241 s amyloid b
3	322	91.7	770	1	A4_MACFA	P53601 m amyloid b
4	322	91.7	770	1	A4_PIG	P79307 s amyloid b
5	321	91.5	770	1	A4_RAT	P08592 r amyloid b
6	319	90.9	770	1	A4_CAVPO	Q60495 c amyloid b
7	317	90.3	770	1	A4_MOUSE	P12023 m amyloid b
8	304	86.6	76	1	A4_MACMU	P29216 macaca mula
9	238	67.8	763	1	APP2_HUMAN	Q06481 homo sapien
10	238	67.8	765	1	APP2_RAT	P15943 rattus norv
11	236	67.2	737	1	A4_FUGRU	O93279 fugu rubrip
12	195.5	55.7	780	1	A4_TETFL	O73683 tetraodon f
13	169	48.1	252	1	SPT2_HUMAN	O43291 homo sapien
14	168	47.9	55	1	ISH1_STOHE	P31713 stoichactis
15	161	45.9	252	1	SPT2_MOUSE	Q9wu03 mus musculu
16	158	45.0	55	1	ISH2_STOHE	P81129 stoichactis
17	158	45.0	58	1	ISIK_HELPO	P00994 helix pomat
18	158	45.0	133	1	EPPI_HUMAN	O95925 homo sapien
19	158	45.0	197	1	MCPI_MELCP	P82968 melithaea c
20	155	44.2	3137	1	CA36_CHICK	P15989 gallus gall
21	153	43.6	67	1	IBPC_BOVIN	P00976 bos taurus
22	153	43.6	100	1	BPT1_BOVIN	P00974 bos taurus
23	153	43.6	302	1	TFPI_RAT	Q02445 rattus norv
24	150	42.7	60	1	IVB2_DABRU	P00990 daboia russ
25	150	42.7	123	1	IATR_SHEEP	P13371 ovis aries
26	149	42.5	349	1	AMBP_MESAU	Q60559 mesocricetu
27	148	42.2	352	1	AMBP_BOVIN	P00978 bos taurus
28	147	41.9	133	1	EPPI_MACMU	Q9bdl1 macaca mula
29	147	41.9	337	1	AMBP_PIG	P04366 sus scrofa
30	147	41.9	349	1	AMBP_MOUSE	Q07456 mus musculu
31	146	41.6	62	1	IP52_ANESU	P10280 anemonia su
32	146	41.6	230	1	TFP2_MOUSE	O35536 mus musculu
33	146	41.6	346	1	AMBP_MERUN	Q62577 meriones un
34	146	41.6	3176	1	CA36_HUMAN	P12111 homo sapien
35	145	41.3	64	1	SPT3_HUMAN	P49223 homo sapien
36	145	41.3	83	1	ELAC_MACEU	O62845 macropus eu
37	144	41.0	60	1	IBPS_BOVIN	P00975 bos taurus
38	144	41.0	507	1	SPT1_MOUSE	Q9r097 mus musculu
39	143	40.7	58	1	AXP1_ANTAF	P81547 anthopleura
40	143	40.7	349	1	AMBP_RAT	Q64240 rattus norv
41	143	40.7	352	1	AMBP_HUMAN	P02760 homo sapien
42	142	40.5	100	1	BPT2_BOVIN	P04815 bos taurus
43	142	40.5	123	1	IATR_HORSE	P04365 equus cabal
44	142	40.5	304	1	TFPI_MACMU	Q28864 macaca mula
45	141	40.2	306	1	TFPI_MOUSE	O54819 mus musculu

ALIGNMENTS

RESULT 1
A4_HUMAN
ID A4_HUMAN STANDARD; PRT; 770 AA.
AC P05067; P09000; P78438; Q13764; Q13778; Q13793; Q16011; Q16014;
AC Q16019; Q16020; Q9BT38; Q9UCA9; Q9UCB6; Q9UCC8; Q9UCD1; Q9UQ58;
DT 13-AUG-1987 (Rel. 05, Created)
DT 01-NOV-1991 (Rel. 20, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Amyloid beta A4 protein precursor (APP) (ABPP) (Alzheimer's disease
DE amyloid protein) (Cerebral vascular amyloid peptide) (CVAP) (Protease
DE nexin-II) (PN-II) (APPI) (PreA4) [Contains: Soluble APP-alpha (S-APP-
DE alpha); Soluble APP-beta (S-APP-beta); C99; Beta-amyloid protein 42
DE (Beta-APP42); Beta-amyloid protein 40 (Beta-APP40); C83; P3(42);
DE P3(40); Gamma-CTF(59) (Gamma-secretase C-terminal fragment 59)
DE (Amyloid intracellular domain 59) (AID(59)); Gamma-CTF(57) (Gamma-
DE secretase C-terminal fragment 57) (Amyloid intracellular domain 57)
DE (AID(57)); Gamma-CTF(50) (Gamma-secretase C-terminal fragment 50)
DE (Amyloid intracellular domain 50) (AID(50)); C31].
GN APP OR A4 OR AD1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM APP695).
RC TISSUE=Brain;
RX MEDLINE=87144572; PubMed=2881207;
RA Kang J., Lemaire H.-G., Unterbeck A., Salbaum J.M., Masters C.L.,
RA Grzeschik K.-H., Multhaup G., Beyreuther K., Mueller-Hill B.;
RT "The precursor of Alzheimer's disease amyloid A4 protein resembles a
RT cell-surface receptor.";
RL Nature 325:733-736(1987).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM APP751).
RC TISSUE=Brain;
RX MEDLINE=88122639; PubMed=2893289;
RA Ponte P., Gonzalez-Dewhitt P., Schilling J., Miller J., Hsu D.,
RA Greenberg B., Davis K., Wallace W., Lieberburg I., Fuller F.,
RA Cordell B.;
RT "A new A4 amyloid mRNA contains a domain homologous to serine
RT proteinase inhibitors.";
RL Nature 331:525-527(1988).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM APP695).
RX MEDLINE=89128427; PubMed=2783775;
RA Lemaire H.-G., Salbaum J.M., Multhaup G., Kang J., Bayney R.M.,
RA Unterbeck A., Beyreuther K., Mueller-Hill B.;
RT "The PreA4(695) precursor protein of Alzheimer's disease A4 amyloid
RT is encoded by 16 exons.";
RL Nucleic Acids Res. 17:517-522(1989).
RN [4]
RP SEQUENCE FROM N.A. (ISOFORM APP770).
RX MEDLINE=90236318; PubMed=2110105;
RA Yoshikai S.-I., Sasaki H., Doh-Ura K., Furuya H., Sakaki Y.;
RT "Genomic organization of the human amyloid beta-protein precursor
RT gene.";

RL Gene 87:257-263(1990).
RN [5]
RP ERRATUM, AND REVISIONS.
RA Yoshikai S.-I., Sasaki H., Doh-ura K., Furuya H., Sakaki Y.;
RL Gene 102:291-292(1991).
RN [6]
RP SEQUENCE FROM N.A. (ISOFORM L-APP733).
RC TISSUE=Leukocyte;
RX MEDLINE=92268136; PubMed=1587857;
RA Koenig G., Moenning U., Czech C., Prior R., Banati R.,
RA Schreiter-Gasser U., Bauer J., Masters C.L., Beyreuther K.;
RT "Identification and differential expression of a novel alternative
RT splice isoform of the beta A4 amyloid precursor protein (APP) mRNA in
RT leukocytes and brain microglial cells.";
RL J. Biol. Chem. 267:10804-10809(1992).
RN [7]
RP SEQUENCE FROM N.A. (ISOFORM APP770).
RX MEDLINE=97263807; PubMed=9108164;
RA Hattori M., Tsukahara F., Furuhata Y., Tanahashi H., Hirose M.,
RA Saito M., Tsukuni S., Sakaki Y.;
RT "A novel method for making nested deletions and its application for
RT sequencing of a 300 kb region of human APP locus.";
RL Nucleic Acids Res. 25:1802-1808(1997).
RN [8]
RP SEQUENCE FROM N.A. (ISOFORM APP639).
RC TISSUE=Brain;
RX MEDLINE=22744650; PubMed=12859342;
RA Tang K., Wang C., Shen C., Sheng S., Ravid R., Jing N.;
RT "Identification of a novel alternative splicing isoform of human
RT amyloid precursor protein gene, APP639.";
RL Eur. J. Neurosci. 18:102-108(2003).
RN [9]
RP SEQUENCE FROM N.A. (ISOFORM APP305).
RC TISSUE=Pancreas;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [10]
RP SEQUENCE OF 1-10 FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=89016647; PubMed=3140222;
RA Schon E.A., Mita S., Sadlock J., Herbert J.;
RT "A cDNA specifying the human amyloid beta precursor protein (ABPP)
RT encodes a 95-kDa polypeptide.";
RL Nucleic Acids Res. 16:9351-9351(1988).
RN [11]
RP ERRATUM, AND REVISIONS.
RA Mita S., Sadlock J., Herbert J., Schon E.A.;
RL Nucleic Acids Res. 16:11402-11402(1988).
RN [12]
RP SEQUENCE OF 1-75 FROM N.A.
RX MEDLINE=89165870; PubMed=2538123;
RA La Fauci G., Lahiri D.K., Salton S.R., Robakis N.K.;
RT "Characterization of the 5'-end region and the first two exons of the
RT beta-protein precursor gene.";
RL Biochem. Biophys. Res. Commun. 159:297-304(1989).
RN [13]
RP SEQUENCE OF 18-50.
RC TISSUE=Fibroblast;
RX MEDLINE=87250462; PubMed=3597385;
RA van Nostrand W.E., Cunningham D.D.;
RT "Purification of protease nexin II from human fibroblasts.";
RL J. Biol. Chem. 262:8508-8514(1987).
RN [14]
RP PARTIAL SEQUENCE FROM N.A. (ISOFORM APP751).
RC TISSUE=Brain;
RX MEDLINE=89346754; PubMed=2569763;
RA de Sauvage F., Octave J.N.;
RT "A novel mRNA of the A4 amyloid precursor gene coding for a possibly
RT secreted protein.";
RL Science 245:651-653(1989).
RN [15]
RP PARTIAL SEQUENCE FROM N.A. (ISOFORM APP695).
RC TISSUE=Brain;
RX MEDLINE=87231971; PubMed=3035574;
RA Robakis N.K., Ramakrishna N., Wolfe G., Wisniewski H.M.;
RT "Molecular cloning and characterization of a cDNA encoding the
RT cerebrovascular and the neuritic plaque amyloid peptides.";
RL Proc. Natl. Acad. Sci. U.S.A. 84:4190-4194(1987).
RN [16]
RP SEQUENCE OF 286-366 FROM N.A.
RX MEDLINE=88122640; PubMed=2893290;
RA Tanzi R.E., McClatchey A.I., Lamperti E.D., Villa-Komaroff L.,
RA Gusella J.F., Neve R.L.;
RT "Protease inhibitor domain encoded by an amyloid protein precursor
RT mRNA associated with Alzheimer's disease.";
RL Nature 331:528-530(1988).
RN [17]
RP SEQUENCE OF 287-367 FROM N.A.
RX MEDLINE=88122641; PubMed=2893291;
RA Kitaguchi N., Takahashi Y., Tokushima Y., Shiojiri S., Ito H.;
RT "Novel precursor of Alzheimer's disease amyloid protein shows
RT protease inhibitory activity.";
RL Nature 331:530-532(1988).
RN [18]
RP SEQUENCE OF 507-770 FROM N.A.
RC TISSUE=Brain cortex;
RX MEDLINE=88124954; PubMed=2893379;
RA Zain S.B., Salim M., Chou W.G., Sajdel-Sulkowska E.M., Majocha R.E.,
RA Marotta C.A.;
RT "Molecular cloning of amyloid cDNA derived from mRNA of the Alzheimer
RT disease brain: coding and noncoding regions of the fetal precursor
RT mRNA are expressed in the cortex.";
RL Proc. Natl. Acad. Sci. U.S.A. 85:929-933(1988).
RN [19]
RP SEQUENCE OF 523-555, AND COLLAGEN-BINDING DOMAIN.
RX MEDLINE=96139497; PubMed=8576160;
RA Beher D., Hesse L., Masters C.L., Multhaup G.;
RT "Regulation of amyloid protein precursor (APP) binding to collagen and
RT mapping of the binding sites on APP and collagen type I.";
RL J. Biol. Chem. 271:1613-1620(1996).
RN [20]
RP SEQUENCE OF 655-737 FROM N.A., AND VARIANTS AD PHE-717; AD ILE-717
RP AND AD GLY-717.
RX MEDLINE=93236601; PubMed=8476439;
RA Denman R.B., Rosenzcwaig R., Miller D.L.;
RT "A system for studying the effect(s) of familial Alzheimer disease
RT mutations on the processing of the beta-amyloid peptide precursor.";
RL Biochem. Biophys. Res. Commun. 192:96-103(1993).
RN [21]
RP SEQUENCE OF 656-737 FROM N.A.
RX MEDLINE=89392030; PubMed=2675837;
RA Johnstone E.M., Chaney M.O., Moore R.E., Ward K.E., Norris F.H.,
RA Little S.P.;
RT "Alzheimer's disease amyloid peptide is encoded by two exons and shows
RT similarity to soybean trypsin inhibitor.";
RL Biochem. Biophys. Res. Commun. 163:1248-1255(1989).
RN [22]

```
  Query Match             92.9%;  Score 326;  DB 1;  Length 770;
  Best Local Similarity   93.4%;  Pred. No. 4e-31;
  Matches   57;  Conservative    1;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 EVVREVCSEQAETGPCRAAIYHWYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMAVCGSA 60
              |||||||||||||||||  |  ||||||||||||||||||||||||||||||||||||||
Db        285 EVVREVCSEQAETGPCRAMISRWYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMAVCGSA 344

Qy         61 I 61
              :
Db        345 M 345


RESULT 2
A4_SAISC
ID   A4_SAISC       STANDARD;      PRT;   751 AA.
AC   Q95241;
DT   15-DEC-1998 (Rel. 37, Created)
DT   15-DEC-1998 (Rel. 37, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Amyloid beta A4 protein precursor (APP) (Alzheimer's disease amyloid
DE   protein homolog) [Contains: Soluble APP-alpha (S-APP-alpha); Soluble
DE   APP-beta (S-APP-beta); C99; Beta-amyloid protein 42 (Beta-APP42);
DE   Beta-amyloid protein 40 (Beta-APP40); C83; P3(42); P3(40); Gamma-
DE   CTF(59) (Gamma-secretase C-terminal fragment 59); Gamma-CTF(57)
DE   (Gamma-secretase C-terminal fragment 57); Gamma-CTF(50) (Gamma-
DE   secretase C-terminal fragment 50); C31].
GN   APP.
OS   Saimiri sciureus (Common squirrel monkey).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Cebinae; Saimiri.
OX   NCBI_TaxID=9521;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Kidney, and Liver;
RX   MEDLINE=96108492; PubMed=8532114;
RA   Levy E., Amorim A., Frangione B., Walker L.C.;
RT   "Beta-amyloid precursor protein gene in squirrel monkeys with
RT   cerebral amyloid angiopathy.";
RL   Neurobiol. Aging 16:805-808(1995).
CC   -!- FUNCTION: Functions as a cell surface receptor and performs
CC       physiological functions on the surface of neurons relevant to
CC       neurite growth, neuronal adhesion and axonogenesis. Involved in
CC       cell mobility and transcription regulation through protein-protein
CC       interactions (By similarity). Can promote transcription activation
CC       through binding to APBB1/Tip60 and inhibit Notch signaling through
CC       interaction with Numb (By similarity). Couples to apoptosis-
CC       inducing pathways such as those mediated by G(O) and JIP (By
CC       similarity). Inhibits G(0) alpha ATPase activity (By similarity).
CC       Acts as a kinesin I membrane receptor, mediating the axonal
CC       transport of beta-secretase and presenilin 1 (By similarity). May
CC       be involved in copper homeostasis/oxidative stress through copper
CC       ion reduction. In vitro, copper-metallated APP induces neuronal
CC       death directly or is potentiated through Cu(II)-mediated low-
CC       density lipoprotein oxidation (By similarity). Can regulate
CC       neurite outgrowth through binding to components of the
CC       extracellular matrix such as heparin and collagen I and IV (By
CC       similarity). The splice isoforms that contain the BPTI domain
CC       possess protease inhibitor activity (By similarity).
CC   -!- FUNCTION: Beta-amyloid peptides are lipophilic metal chelators
CC       with metal-reducing activity. Bind transient metals such as
CC       copper, zinc and iron (By similarity).
CC   -!- FUNCTION: The gamma-CTF peptides as well as the caspase-cleaved
CC       peptides, including C31, are potent enhancers of neuronal
CC       apoptosis (By similarity).
CC   -!- SUBUNIT: Binds, via its C-terminal, to the PID domain of several
CC       cytoplasmic proteins, including APBB family members, the APBA
CC       family, MAPK8IP1, and SHC1, Numb and Dab1 (By similarity). Binding
CC       to Dab1 inhibits its serine phosphorylation (By similarity). Also
CC       interacts with GPCR-like protein BPP, FPRL1, APPBP1, IB1, KNS2
CC       (via its TPR domains) (By similarity), APPBP2 (via BaSS) and DDB1.
CC       In vitro, it binds MAPT via the MT-binding domains (By
CC       similarity). Associates with microtubules in the presence of ATP
CC       and in a kinesin-dependent manner (By similarity).
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein. Cell surface
CC       protein that rapidly becomes internalized via clathrin-coated
CC       pits. During maturation, the immature APP (N-glycosylated in the
CC       endoplasmic reticulum) moves to the Golgi complex where complete
CC       maturation occurs (O-glycosylated and sulfated). After alpha-
CC       secretase cleavage, soluble APP is released into the extracellular
CC       space and the C-terminal is internalized to endosomes and
CC       lysosomes. Some APP accumulates in secretory transport vesicles
CC       leaving the late Golgi compartment and returns to the cell
CC       surface. Gamma-CTF(59) peptide is located to both the cytoplasm
CC       and nuclei of neurons (By similarity).
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=2;
CC         Comment=Additional isoforms seem to exist;
CC       Name=APP770;
CC         IsoId=Q95241-1; Sequence=Displayed;
CC       Name=APP695;
CC         IsoId=Q95241-2; Sequence=Not described;
CC   -!- DOMAIN: The basolateral sorting signal (BaSS) is required for
CC       sorting of membrane proteins to the basolateral surface of
CC       epithelial cells (By similarity).
CC   -!- DOMAIN: The NPXY sequence motif found in many tyrosine-
CC       phosphorylated proteins is required for the specific binding of
CC       the PID domain. However additional amino acids either N- or C-
CC       terminal to the NPXY motif are often required for complete
CC       interaction. The PID domain-containing proteins which bind APP
CC       require the YENPTY motif for full interaction. These interactions
CC       are independent of phosphorylation on the terminal tyrosine
CC       residue. The NPXY site is also involved in clathrin-mediated
CC       endocytosis (By similarity).
CC   -!- PTM: Proteolytically processed under normal cellular conditions.
CC       Cleavage by alpha-secretase or alternatively by beta-secretase
CC       leads to generation and extracellular release of soluble APP
CC       peptides, S-APP-alpha and S-APP-beta, respectively, and the
CC       retention of corresponding membrane-anchored C-terminal fragments,
CC       C83 and C99. Subsequent processing of C83 by gamma-secretase
CC       yields P3 peptides. This is the major secretory pathway and is
CC       nonamyloidogenic. Alternatively, presenilin/nicastrin-mediated
CC       gamma-secretase processing of C99 releases the amyloid beta
CC       proteins, amyloid-beta 40 (Abeta40) and amyloid-beta 42 (Abeta42),
CC       major components of amyloid plaques, and the cytotoxic C-terminal
CC       fragments, gamma-CTF(50), gamma-CTF(57) and gamma-CTF(59) (By
CC       similarity).
CC   -!- PTM: Proteolytically cleaved by caspases during neuronal apoptosis
CC       (By similarity). Cleavage at Asp-720 by either caspase-3, -8 or -9
CC       results in the production of the neurotoxic C31 peptide and the
CC       increased production of beta-amyloid peptides (By similarity).
CC   -!- PTM: N- and O-glycosylated (By similarity).
CC   -!- PTM: Phosphorylation in the C-terminal on tyrosine, threonine and
CC       serine residues is neuron-specific. Phosphorylation can affect APP
CC       processing, neuronal differentiation and interaction with other
CC       proteins (By similarity).
CC   -!- MISCELLANEOUS: Chelation of metal ions, notably copper, iron and
CC       zinc, can induce histidine-bridging between beta-amyloid molecules
CC       resulting in beta-amyloid-metal aggregates (By similarity).
CC       Extracellular zinc-binding increases binding of heparin to APP and
CC       inhibits collagen-binding (By similarity).
CC   -!- SIMILARITY: Belongs to the APP family.
CC   -!- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; S81024; AAD14347.1; -.
DR   HSSP; P05067; 1AAP.
DR   InterPro; IPR008155; A4_APP.
```

```
DR   InterPro; IPR008154; A4_extra.
DR   InterPro; IPR001255; Beta-APP.
DR   InterPro; IPR002223; Kunitz_BPTI.
DR   Pfam; PF02177; A4_EXTRA; 1.
DR   Pfam; PF03494; Beta-APP; 1.
DR   Pfam; PF00014; Kunitz_BPTI; 1.
DR   PRINTS; PR00203; AMYLOIDA4.
DR   PRINTS; PR00759; BASICPTASE.
DR   ProDom; PD000222; Kunitz_BPTI; 1.
DR   SMART; SM00006; A4_EXTRA; 1.
DR   SMART; SM00131; KU; 1.
DR   PROSITE; PS00319; A4_EXTRA; 1.
DR   PROSITE; PS00320; A4_INTRA; 1.
DR   PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR   PROSITE; PS50279; BPTI_KUNITZ_2; 1.
KW   Apoptosis; Endocytosis; Cell adhesion; Serine protease inhibitor;
KW   Coated pits; Neurone; Heparin-binding; Metal-binding; Copper; Iron;
KW   Zinc; Signal; Transmembrane; Glycoprotein; Phosphorylation;
KW   Proteoglycan; Amyloid; Alternative splicing.
FT   SIGNAL       1    17       BY SIMILARITY.
FT   CHAIN       18   751       A4 PROTEIN.
FT   CHAIN       18   668       SOLUBLE APP-ALPHA (POTENTIAL).
FT   CHAIN       18   652       SOLUBLE APP-BETA (POTENTIAL).
FT   CHAIN      653   751       C99 (POTENTIAL).
FT   CHAIN      653   694       BETA-AMYLOID PROTEIN 42 (POTENTIAL).
FT   CHAIN      653   692       BETA-AMYLOID PROTEIN 40 (POTENTIAL).
FT   CHAIN      669   751       C83 (POTENTIAL).
FT   CHAIN      669   694       P3(42) (POTENTIAL).
FT   CHAIN      669   692       P3(40) (POTENTIAL).
FT   CHAIN      693   751       GAMMA-CTF(59) (POTENTIAL).
FT   CHAIN      695   751       GAMMA-CTF(57) (POTENTIAL).
FT   CHAIN      702   751       GAMMA-CTF(50) (POTENTIAL).
FT   CHAIN      721   751       C31 (POTENTIAL).
FT   DOMAIN      18   680       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM   681   704       POTENTIAL.
FT   DOMAIN     705   751       CYTOPLASMIC (POTENTIAL).
FT   DOMAIN      96   110       HEPARIN-BINDING (BY SIMILARITY).
FT   DOMAIN     181   188       ZINC-BINDING (BY SIMILARITY).
FT   DOMAIN     291   341       BPTI/KUNITZ INHIBITOR.
FT   DOMAIN     316   344       HEPARIN-BINDING (BY SIMILARITY).
FT   DOMAIN     363   428       HEPARIN-BINDING (BY SIMILARITY).
FT   DOMAIN     504   521       COLLAGEN-BINDING (BY SIMILARITY).
FT   DOMAIN     713   732       INTERACTION WITH G(O)-ALPHA
FT                              (BY SIMILARITY).
FT   DOMAIN     230   260       ASP/GLU-RICH (ACIDIC).
FT   DOMAIN     274   280       POLY-THR.
FT   SITE       144   144       REQUIRED FOR COPPER(II) REDUCTION
FT                              (BY SIMILARITY).
FT   ACT_SITE   301   302       REACTIVE BOND.
FT   SITE       652   653       CLEAVAGE (BY BETA-SECRETASE)
FT                              (BY SIMILARITY).
FT   SITE       653   654       CLEAVAGE (BY CASPASE-6) (BY SIMILARITY).
FT   SITE       668   669       CLEAVAGE (BY ALPHA-SECRETASE)
FT                              (BY SIMILARITY).
FT   SITE       685   685       INVOLVED IN FREE RADICAL PROPAGATION
FT                              (BY SIMILARITY).
FT   SITE       687   687       INVOLVED IN OXIDATIVE REACTIONS
FT                              (BY SIMILARITY).
FT   SITE       692   693       CLEAVAGE (BY GAMMA-SECRETASE; SITE 1)
FT                              (BY SIMILARITY).
FT   SITE       694   695       CLEAVAGE (BY GAMMA-SECRETASE; SITE 2)
FT                              (BY SIMILARITY).
FT   SITE       701   702       CLEAVAGE (BY GAMMA-SECRETASE; SITE 3)
FT                              (BY SIMILARITY).
FT   SITE       705   715       BASOLATERAL SORTING SIGNAL
FT                              (BY SIMILARITY).
FT   SITE       720   721       CLEAVAGE (BY CASPASES-3,-6,-8 OR -9)
FT                              (BY SIMILARITY).
FT   SITE       738   741       ENDOCYTOSIS SIGNAL.
FT   SITE       740   743       NPXY MOTIF.

  Query Match             92.6%;  Score 325;  DB 1;  Length 751;
  Best Local Similarity   93.4%;  Pred. No. 5.1e-31;

  Matches   57;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 EVVREVCSEQAETGPCRAAIYHWYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMAVCGSA 60
              |||||||||||||||||| | ||||||||||||||||||||||||||||||||||||||
Db        285 EVVREVCSEQAETGPCRAMISRWYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMAVCGSV 344

Qy         61 I 61
              |
Db        345 I 345


RESULT 3
A4_MACFA
ID   A4_MACFA       STANDARD;      PRT;   770 AA.
AC   P53601; Q95KN7;
DT   01-OCT-1996 (Rel. 34, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   Amyloid beta A4 protein precursor (APP) (ABPP) (Alzheimer's disease
DE   amyloid protein homolog) [Contains: Soluble APP-alpha (S-APP-alpha);
DE   Soluble APP-beta (S-APP-beta); C99; Beta-amyloid protein 42 (Beta-
DE   APP42); Beta-amyloid protein 40 (Beta-APP40); C83; P3(42); P3(40);
DE   Gamma-CTF(59) (Gamma-secretase C-terminal fragment 59); Gamma-CTF(57)
DE   (Gamma-secretase C-terminal fragment 57); Gamma-CTF(50) (Gamma-
DE   secretase C-terminal fragment 50); C31].
GN   APP.
OS   Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC   Cercopithecinae; Macaca.
OX   NCBI_TaxID=9541;
RN   [1]
RP   SEQUENCE FROM N.A. (ISOFORMS APP695 AND APP770).
RC   TISSUE=Cerebellum;
RX   MEDLINE=91273117; PubMed=1905108;
RA   Podlisny M.B., Tolan D.R., Selkoe D.J.;
RT   "Homology of the amyloid beta protein precursor in monkey and human
RT   supports a primate model for beta amyloidosis in Alzheimer's
RT   disease.";
RL   Am. J. Pathol. 138:1423-1435(1991).
CC   -!- FUNCTION: Functions as a cell surface receptor and performs
CC       physiological functions on the surface of neurons relevant to
CC       neurite growth, neuronal adhesion and axonogenesis. Involved in
CC       cell mobility and transcription regulation through protein-protein
CC       interactions (By similarity). Can promote transcription activation
CC       through binding to APBB1/Tip60 and inhibit Notch signaling through
CC       interaction with Numb (By similarity). Couples to apoptosis-
CC       inducing pathways such as those mediated by G(O) and JIP (By
CC       similarity). Inhibits G(0) alpha ATPase activity (By similarity).
CC       Acts as a kinesin I membrane receptor, mediating the axonal
CC       transport of beta-secretase and presenilin 1 (By similarity). May
CC       be involved in copper homeostasis/oxidative stress through copper
CC       ion reduction. In vitro, copper-metallated APP induces neuronal
CC       death directly or is potentiated through Cu(II)-mediated low-
CC       density lipoprotein oxidation (By similarity). Can regulate
CC       neurite outgrowth through binding to components of the
CC       extracellular matrix such as heparin and collagen I and IV (By
CC       similarity). The splice isoforms that contain the BPTI domain
CC       possess protease inhibitor activity (By similarity).
CC   -!- FUNCTION: Beta-amyloid peptides are lipophilic metal chelators
CC       with metal-reducing activity. Bind transient metals such as
CC       copper, zinc and iron (By similarity).
CC   -!- FUNCTION: The gamma-CTF peptides as well as the caspase-cleaved
CC       peptides, including C31, are potent enhancers of neuronal
CC       apoptosis (By similarity).
CC   -!- SUBUNIT: Binds, via its C-terminal, to the PID domain of several
CC       cytoplasmic proteins, including APBB family members, the APBA
CC       family, MAPK8IP1, and SHC1, Numb and Dab1 (By similarity). Binding
CC       to Dab1 inhibits its serine phosphorylation (By similarity). Also
CC       interacts with GPCR-like protein BPP, FPRL1, APPBP1, IB1, KNS2
CC       (via its TPR domains) (By similarity), APPBP2 (via BaSS) and DDB1.
CC       In vitro, it binds MAPT via the MT-binding domains (By
CC       similarity). Associates with microtubules in the presence of ATP
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CC       and in a kinesin-dependent manner (By similarity).
CC    -!- SUBCELLULAR LOCATION: Type I membrane protein. Cell surface
CC       protein that rapidly becomes internalized via clathrin-coated
CC       pits. During maturation, the immature APP (N-glycosylated in the
CC       endoplasmic reticulum) moves to the Golgi complex where complete
CC       maturation occurs (O-glycosylated and sulfated). After alpha-
CC       secretase cleavage, soluble APP is released into the extracellular
CC       space and the C-terminal is internalized to endosomes and
CC       lysosomes. Some APP accumulates in secretory transport vesicles
CC       leaving the late Golgi compartment and returns to the cell
CC       surface. Gamma-CTF(59) peptide is located to both the cytoplasm
CC       and nuclei of neurons (By similarity).
CC    -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=2;
CC         Comment=Additional isoforms seem to exist;
CC       Name=APP770;
CC         IsoId=P53601-1; Sequence=Displayed;
CC       Name=APP695;
CC         IsoId=P53601-2; Sequence=VSP_000010, VSP_000011;
CC    -!- DOMAIN: The basolateral sorting signal (BaSS) is required for
CC       sorting of membrane proteins to the basolateral surface of
CC       epithelial cells (By similarity).
CC    -!- DOMAIN: The NPXY sequence motif found in many tyrosine-
CC       phosphorylated proteins is required for the specific binding of
CC       the PID domain. However additional amino acids either N- or C-
CC       terminal to the NPXY motif are often required for complete
CC       interaction. The PID domain-containing proteins which bind APP
CC       require the YENPTY motif for full interaction. These interactions
CC       are independent of phosphorylation on the terminal tyrosine
CC       residue. The NPXY site is also involved in clathrin-mediated
CC       endocytosis (By similarity).
CC    -!- PTM: Proteolytically processed under normal cellular conditions.
CC       Cleavage by alpha-secretase or alternatively by beta-secretase
CC       leads to generation and extracellular release of soluble APP
CC       peptides, S-APP-alpha and S-APP-beta, respectively, and the
CC       retention of corresponding membrane-anchored C-terminal fragments,
CC       C83 and C99. Subsequent processing of C83 by gamma-secretase
CC       yields P3 peptides. This is the major secretory pathway and is
CC       nonamyloidogenic. Alternatively, presenilin/nicastrin-mediated
CC       gamma-secretase processing of C99 releases the amyloid beta
CC       proteins, amyloid-beta 40 (Abeta40) and amyloid-beta 42 (Abeta42),
CC       major components of amyloid plaques, and the cytotoxic C-terminal
CC       fragments, gamma-CTF(50), gamma-CTF(57) and gamma-CTF(59) (By
CC       similarity).
CC    -!- PTM: Proteolytically cleaved by caspases during neuronal apoptosis
CC       (By similarity). Cleavage at Asp-739 by either caspase-3, -8 or -9
CC       results in the production of the neurotoxic C31 peptide and the
CC       increased production of beta-amyloid peptides (By similarity).
CC    -!- PTM: N- and O-glycosylated (By similarity).
CC    -!- PTM: Phosphorylation in the C-terminal on tyrosine, threonine and
CC       serine residues is neuron-specific. Phosphorylation can affect APP
CC       processing, neuronal differentiation and interaction with other
CC       proteins (By similarity).
CC    -!- MISCELLANEOUS: Chelation of metal ions, notably copper, iron and
CC       zinc, can induce histidine-bridging between beta-amyloid molecules
CC       resulting in beta-amyloid-metal aggregates (By similarity).
CC       Extracellular zinc-binding increases binding of heparin to APP and
CC       inhibits collagen-binding (By similarity).
CC    -!- SIMILARITY: Belongs to the APP family.
CC    -!- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
CC    ----------------------------------------------------------------------
CC    This SWISS-PROT entry is copyright. It is produced through a collaboration
CC    between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC    the European Bioinformatics Institute. There are no restrictions on its
CC    use by non-profit institutions as long as its content is in no way
CC    modified and this statement is not removed. Usage by and for commercial
CC    entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC    or send an email to license@isb-sib.ch).
CC    ----------------------------------------------------------------------
DR    EMBL; M58727; AAA36829.1; -.
DR    EMBL; M58726; AAA36828.1; -.
DR    HSSP; P05067; 1AAP.
DR    InterPro; IPR008155; A4_APP.
DR    InterPro; IPR008154; A4_extra.
DR    InterPro; IPR001255; Beta-APP.
DR    InterPro; IPR002223; Kunitz_BPTI.
DR    Pfam; PF02177; A4_EXTRA; 1.
DR    Pfam; PF03494; Beta-APP; 1.
DR    Pfam; PF00014; Kunitz_BPTI; 1.
DR    PRINTS; PR00203; AMYLOIDA4.
DR    PRINTS; PR00759; BASICPTASE.
DR    ProDom; PD000222; Kunitz_BPTI; 1.
DR    SMART; SM00006; A4_EXTRA; 1.
DR    SMART; SM00131; KU; 1.
DR    PROSITE; PS00319; A4_EXTRA; 1.
DR    PROSITE; PS00320; A4_INTRA; 1.
DR    PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR    PROSITE; PS50279; BPTI_KUNITZ_2; 1.
KW    Apoptosis; Endocytosis; Cell adhesion; Serine protease inhibitor;
KW    Coated pits; Neurone; Heparin-binding; Metal-binding; Copper; Iron;
KW    Zinc; Signal; Transmembrane; Glycoprotein; Phosphorylation;
KW    Proteoglycan; Alternative splicing; Amyloid.
FT    SIGNAL        1     17       BY SIMILARITY.
FT    CHAIN        18    770       AMYLOID BETA A4 PROTEIN.
FT    CHAIN        18    687       SOLUBLE APP-ALPHA (POTENTIAL).
FT    CHAIN        18    671       SOLUBLE APP-BETA (POTENTIAL).
FT    CHAIN       672    770       C99 (POTENTIAL).
FT    CHAIN       672    713       BETA-AMYLOID PROTEIN 42 (POTENTIAL).
FT    CHAIN       672    711       BETA-AMYLOID PROTEIN 40 (POTENTIAL).
FT    CHAIN       688    770       C83 (POTENTIAL).
FT    CHAIN       688    713       P3(42) (POTENTIAL).
FT    CHAIN       688    711       P3(40) (POTENTIAL).
FT    CHAIN       712    770       GAMMA-CTF(59) (POTENTIAL).
FT    CHAIN       714    770       GAMMA-CTF(57) (POTENTIAL).
FT    CHAIN       721    770       GAMMA-CTF(50) (POTENTIAL).
FT    CHAIN       740    770       C31 (POTENTIAL).
FT    DOMAIN       18    699       EXTRACELLULAR (POTENTIAL).
FT    TRANSMEM    700    723       POTENTIAL.
FT    DOMAIN      724    770       CYTOPLASMIC (POTENTIAL).
FT    DOMAIN       96    110       HEPARIN-BINDING (BY SIMILARITY).
FT    DOMAIN      181    188       ZINC-BINDING (BY SIMILARITY).
FT    DOMAIN      291    341       BPTI/KUNITZ INHIBITOR.
FT    DOMAIN      391    423       HEPARIN-BINDING (BY SIMILARITY).
FT    DOMAIN      491    522       HEPARIN-BINDING (BY SIMILARITY).
FT    DOMAIN      523    540       COLLAGEN-BINDING (BY SIMILARITY).
FT    DOMAIN      732    751       INTERACTION WITH G(O)-ALPHA
FT                                  (BY SIMILARITY).
FT    DOMAIN      230    260       ASP/GLU-RICH (ACIDIC).
FT    DOMAIN      274    280       POLY-THR.
FT    SITE        144    144       REQUIRED FOR COPPER(II) REDUCTION
FT                                  (BY SIMILARITY).
FT    ACT_SITE    301    302       REACTIVE BOND (BY SIMILARITY).
FT    SITE        671    672       CLEAVAGE (BY BETA-SECRETASE)
FT                                  (BY SIMILARITY).
FT    SITE        672    673       CLEAVAGE (BY CASPASE-6) (BY SIMILARITY).
FT    SITE        687    688       CLEAVAGE (BY ALPHA-SECRETASE)
FT                                  (BY SIMILARITY).
FT    SITE        704    704       IMPLICATED IN FREE RADICAL PROPAGATION
FT                                  (BY SIMILARITY).
FT    SITE        706    706       INVOLVED IN OXIDATIVE REACTIONS
FT                                  (BY SIMILARITY).
FT    SITE        711    712       CLEAVAGE (BY GAMMA-SECRETASE; SITE 1)
FT                                  (BY SIMILARITY).
FT    SITE        713    714       CLEAVAGE (BY GAMMA-SECRETASE; SITE 2)
FT                                  (BY SIMILARITY).
FT    SITE        720    721       CLEAVAGE (BY GAMMA-SECRETASE; SITE 3)
FT                                  (BY SIMILARITY).
FT    SITE        724    734       BASOLATERAL SORTING SIGNAL
FT                                  (BY SIMILARITY).
FT    SITE        739    740       CLEAVAGE (BY CASPASES-3,-6,-8 OR -9)

  Query Match             91.7%;  Score 322;  DB 1;  Length 770;
  Best Local Similarity   91.8%;  Pred. No. 1.2e-30;
  Matches   56;  Conservative    1;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 EVVREVCSEQAETGPCRAAIYHWYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMAVCGSA 60
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                    ||||||||||||||||||  |  ||||||||||||||||||||||||||||||||||||
Db        285 EVVREVCSEQAETGPCRAMISRWYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMAVCGSV 344

Qy         61 I 61

Db        345 M 345


RESULT 4
A4_PIG
ID   A4_PIG          STANDARD;      PRT;   770 AA.
AC   P79307; Q29023; Q9TUI0;
DT   01-NOV-1997 (Rel. 35, Created)
DT   10-OCT-2003 (Rel. 42, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Amyloid beta A4 protein precursor (APP) (ABPP) (Alzheimer's disease
DE   amyloid protein homolog) [Contains: Soluble APP-alpha (S-APP-alpha);
DE   Soluble APP-beta (S-APP-beta); C99; Beta-amyloid protein 42 (Beta-
DE   APP42); Beta-amyloid protein 40 (Beta-APP40); C83; P3(42); P3(40);
DE   Gamma-CTF(59) (Gamma-secretase C-terminal fragment 59); Gamma-CTF(57)
DE   (Gamma-secretase C-terminal fragment 57); Gamma-CTF(50) (Gamma-
DE   secretase C-terminal fragment 50); C31].
OS   Sus scrofa (Pig).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX   NCBI_TaxID=9823;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Kimura A., Takahashi T.;
RT   "Amyloid precursor protein 770.";
RL   Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE OF 1-136 FROM N.A.
RC   TISSUE=Small intestine;
RA   Winteroe A.K., Fredholm M.;
RT   "Evaluation and characterization of a porcine small intestine cDNA
RT   library.";
RL   Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   SEQUENCE OF 667-723 FROM N.A.
RC   TISSUE=Brain;
RX   MEDLINE=92017079; PubMed=1656157;
RA   Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
RT   "Conservation of the sequence of the Alzheimer's disease amyloid
RT   peptide in dog, polar bear and five other mammals by cross-species
RT   polymerase chain reaction analysis.";
RL   Brain Res. Mol. Brain Res. 10:299-305(1991).
CC   -!- FUNCTION: Functions as a cell surface receptor and performs
CC       physiological functions on the surface of neurons relevant to
CC       neurite growth, neuronal adhesion and axonogenesis. Involved in
CC       cell mobility and transcription regulation through protein-protein
CC       interactions (By similarity). Can promote transcription activation
CC       through binding to APBB1/Tip60 and inhibit Notch signaling through
CC       interaction with Numb (By similarity). Couples to apoptosis-
CC       inducing pathways such as those mediated by G(O) and JIP (By
CC       similarity). Inhibits G(O) alpha ATPase activity (By similarity).
CC       Acts as a kinesin I membrane receptor, mediating the axonal
CC       transport of beta-secretase and presenilin 1 (By similarity). May
CC       be involved in copper homeostasis/oxidative stress through copper
CC       ion reduction (By similarity). In vitro, copper-metallated APP
CC       induces neuronal death directly or is potentiated through Cu(II)-
CC       mediated low-density lipoprotein oxidation (By similarity). Can
CC       regulate neurite outgrowth through binding to components of the
CC       extracellular matrix such as heparin and collagen I and IV (By
CC       similarity).
CC   -!- FUNCTION: Beta-amyloid peptides are lipophilic metal chelators
CC       with metal-reducing activity. Bind transient metals such as
CC       copper, zinc and iron (By similarity).
CC   -!- FUNCTION: The gamma-CTF peptides as well as the caspase-cleaved
CC       peptides, including C31, are potent enhancers of neuronal
CC       apoptosis (By similarity).
CC   -!- SUBUNIT: Binds, via its C-terminal, to the PID domain of several
CC       cytoplasmic proteins, including APBB family members, the APBA
CC       family, MAPK8IP1, and SHC1, Numb and Dab1 (By similarity). Binding
CC       to Dab1 inhibits its serine phosphorylation (By similarity). Also
CC       interacts with GPCR-like protein BPP, FPRL1, APPBP1, IB1, KNS2
CC       (via its TPR domains) (By similarity), APPBP2 (via BaSS) and DDB1.
CC       In vitro, it binds MAPT via the MT-binding domains (By
CC       similarity). Associates with microtubules in the presence of ATP
CC       and in a kinesin-dependent manner (By similarity).
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein. Cell surface
CC       protein that rapidly becomes internalized via clathrin-coated
CC       pits. During maturation, the immature APP (N-glycosylated in the
CC       endoplasmic reticulum) moves to the Golgi complex where complete
CC       maturation occurs (O-glycosylated and sulfated). After alpha-
CC       secretase cleavage, soluble APP is released into the extracellular
CC       space and the C-terminal is internalized to endosomes and
CC       lysosomes. Some APP accumulates in secretory transport vesicles
CC       leaving the late Golgi compartment and returns to the cell
CC       surface. Gamma-CTF(59) peptide is located to both the cytoplasm
CC       and nuclei of neurons (By similarity).
CC   -!- DOMAIN: The basolateral sorting signal (BaSS) is required for
CC       sorting of membrane proteins to the basolateral surface of
CC       epithelial cells (By similarity).
CC   -!- DOMAIN: The NPXY sequence motif found in many tyrosine-
CC       phosphorylated proteins is required for the specific binding of
CC       the PID domain. However additional amino acids either N- or C-
CC       terminal to the NPXY motif are often required for complete
CC       interaction. The PID domain-containing proteins which bind APP
CC       require the YENPTY motif for full interaction. These interactions
CC       are independent of phosphorylation on the terminal tyrosine
CC       residue. The NPXY site is also involved in clathrin-mediated
CC       endocytosis (By similarity).
CC   -!- PTM: Proteolytically processed under normal cellular conditions.
CC       Cleavage by alpha-secretase or alternatively by beta-secretase
CC       leads to generation and extracellular release of soluble APP
CC       peptides, S-APP-alpha and S-APP-beta, respectively, and the
CC       retention of corresponding membrane-anchored C-terminal fragments,
CC       C83 and C99. Subsequent processing of C83 by gamma-secretase
CC       yields P3 peptides. This is the major secretory pathway and is
CC       nonamyloidogenic. Alternatively, presenilin/nicastrin-mediated
CC       gamma-secretase processing of C99 releases the amyloid beta
CC       proteins, amyloid-beta 40 (Abeta40) and amyloid-beta 42 (Abeta42),
CC       major components of amyloid plaques, and the cytotoxic C-terminal
CC       fragments, gamma-CTF(50), gamma-CTF(57) and gamma-CTF(59) (By
CC       similarity).
CC   -!- PTM: Proteolytically cleaved by caspases during neuronal apoptosis
CC       (By similarity). Cleavage at Asp-739 by either caspase-3, -8 or -9
CC       results in the production of the neurotoxic C31 peptide and the
CC       increased production of beta-amyloid peptides (By similarity).
CC   -!- PTM: N- and O-glycosylated (By similarity).
CC   -!- PTM: Phosphorylation in the C-terminal on tyrosine, threonine and
CC       serine residues is neuron-specific. Phosphorylation can affect APP
CC       processing, neuronal differentiation and interaction with other
CC       proteins (By similarity).
CC   -!- PTM: Extracellular binding and reduction of copper, results in a
CC       corresponding oxidation of Cys-144 and Cys-158, and the formation
CC       of a disulfide bond (By similarity).
CC   -!- MISCELLANEOUS: Chelation of metal ions, notably copper, iron and
CC       zinc, can induce histidine-bridging between beta-amyloid molecules
CC       resulting in beta-amyloid-metal aggregates (By similarity).
CC       Extracellular zinc-binding increases binding of heparin to APP and
CC       inhibits collagen-binding (By similarity).
CC   -!- SIMILARITY: Belongs to the APP family.
CC   -!- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AB032550; BAA84580.1; -.
DR   EMBL; Z84022; CAB06313.1; -.
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DR   EMBL; X56127; CAA39592.1; -.
DR   HSSP; P05067; 1AAP.
DR   InterPro; IPR008155; A4_APP.
DR   InterPro; IPR008154; A4_extra.
DR   InterPro; IPR002223; Kunitz_BPTI.
DR   Pfam; PF02177; A4_EXTRA; 1.
DR   PRINTS; PR00203; AMYLOIDA4.
DR   PRINTS; PR00759; BASICPTASE.
DR   ProDom; PD000222; Kunitz_BPTI; 1.
DR   SMART; SM00006; A4_EXTRA; 1.
DR   SMART; SM00131; KU; 1.
DR   PROSITE; PS00319; A4_EXTRA; 1.
DR   PROSITE; PS00320; A4_INTRA; 1.
DR   PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR   PROSITE; PS50279; BPTI_KUNITZ_2; 1.
KW   Apoptosis; Endocytosis; Cell adhesion; Serine protease inhibitor;
KW   Coated pits; Neurone; Heparin-binding; Metal-binding; Copper; Iron;
KW   Zinc; Signal; Transmembrane; Glycoprotein; Phosphorylation;
KW   Amyloid.
FT   SIGNAL        1     17       BY SIMILARITY.
FT   CHAIN        18    770       AMYLOID BETA A4 PROTEIN.
FT   CHAIN        18    687       SOLUBLE APP-ALPHA (POTENTIAL).
FT   CHAIN        18    671       SOLUBLE APP-BETA (POTENTIAL).
FT   CHAIN       672    770       C99 (BY SIMILARITY).
FT   CHAIN       672    713       BETA-AMYLOID PROTEIN 42 (BY SIMILARITY).
FT   CHAIN       672    711       BETA-AMYLOID PROTEIN 40 (BY SIMILARITY).
FT   CHAIN       688    770       C83 (BY SIMILARITY).
FT   CHAIN       688    713       P3(42) (BY SIMILARITY).
FT   CHAIN       688    711       P3(40) (BY SIMILARITY).
FT   CHAIN       712    770       GAMMA-CTF(59).
FT   CHAIN       714    770       GAMMA-CTF(57).
FT   CHAIN       721    770       GAMMA-CTF(50) (BY SIMILARITY).
FT   CHAIN       740    770       C31 (DURING APOPTOSIS) (BY SIMILARITY).
FT   DOMAIN       18    699       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    700    723       POTENTIAL.
FT   DOMAIN      724    770       CYTOPLASMIC (POTENTIAL).
FT   DOMAIN       96    110       HEPARIN-BINDING (BY SIMILARITY).
FT   DOMAIN      135    155       COPPER-BINDING (BY SIMILARITY).
FT   DOMAIN      181    188       ZINC-BINDING (BY SIMILARITY).
FT   DOMAIN      291    341       BPTI/KUNITZ INHIBITOR.
FT   DOMAIN      391    423       HEPARIN-BINDING (BY SIMILARITY).
FT   DOMAIN      491    522       HEPARIN-BINDING (BY SIMILARITY).
FT   DOMAIN      523    540       COLLAGEN-BINDING (BY SIMILARITY).
FT   DOMAIN      732    751       INTERACTION WITH G(O)-ALPHA (BY
FT                                SIMILARITY).
FT   DOMAIN      230    260       ASP/GLU-RICH (ACIDIC).
FT   DOMAIN      274    280       POLY-THR.
FT   SITE        144    144       REQUIRED FOR COPPER(II) REDUCTION
FT                                (BY SIMILARITY).
FT   ACT_SITE    301    302       REACTIVE BOND (BY SIMILARITY).
FT   SITE        671    672       CLEAVAGE (BY BETA-SECRETASE)
FT                                (BY SIMILARITY).
FT   SITE        672    673       CLEAVAGE (BY CASPASE-6) (BY SIMILARITY).
FT   SITE        687    688       CLEAVAGE (BY ALPHA-SECRETASE)
FT                                (BY SIMILARITY).
FT   SITE        704    704       IMPLICATED IN FREE RADICAL PROPAGATION
FT                                (BY SIMILARITY).
FT   SITE        706    706       INVOLVED IN OXIDATIVE REACTIONS
FT                                (BY SIMILARITY).
FT   SITE        711    712       CLEAVAGE (BY GAMMA-SECRETASE; SITE 1)
FT                                (BY SIMILARITY).
FT   SITE        713    714       CLEAVAGE (BY GAMMA-SECRETASE; SITE 2)
FT                                (BY SIMILARITY).
FT   SITE        720    721       CLEAVAGE (BY GAMMA-SECRETASE; SITE 3)

  Query Match           91.7%;  Score 322;  DB 1;  Length 770;
  Best Local Similarity  91.8%;  Pred. No. 1.2e-30;
  Matches   56;  Conservative    1;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 EVVREVCSEQAETGPCRAAIYHWYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMAVCGSA 60
              |||||||||||||||| |  ||||||||||||||||||||||||||||||||||||||||
Db        285 EVVREVCSEQAETGPCRAMISRWYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMAVCGSV 344

Qy         61 I 61
              :
Db        345 M 345


RESULT 5
A4_RAT
ID   A4_RAT          STANDARD;      PRT;   770 AA.
AC   P08592;
DT   01-AUG-1988 (Rel. 08, Created)
DT   01-DEC-1992 (Rel. 24, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Amyloid beta A4 protein precursor (APP) (Alzheimer's disease amyloid
DE   protein homolog) (Amyloidogenic glycoprotein) (AG) [Contains: Soluble
DE   APP-alpha (S-APP-alpha); Soluble APP-beta (S-APP-beta); C99; Beta-
DE   amyloid protein 42 (Beta-APP42); Beta-amyloid protein 40 (Beta-APP40);
DE   C83; P3(42); P3(40); Gamma-CTF(59) (Gamma-secretase C-terminal
DE   fragment 59); Gamma-CTF(57) (Gamma-secretase C-terminal fragment 57);
DE   Gamma-CTF(50) (Gamma-secretase C-terminal fragment 50); C31].
GN   APP.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A. (ISOFORM APP695).
RC   TISSUE=Brain;
RX   MEDLINE=88312583; PubMed=2900758;
RA   Shivers B.D., Hilbich C., Multhaup G., Salbaum J.M., Beyreuther K.,
RA   Seeburg P.H.;
RT   "Alzheimer's disease amyloidogenic glycoprotein: expression pattern
RT   in rat brain suggests a role in cell contact.";
RL   EMBO J. 7:1365-1370(1988).
RN   [2]
RP   SEQUENCE OF 289-364 FROM N.A.
RC   TISSUE=Liver;
RX   MEDLINE=89183625; PubMed=2648331;
RA   Kang J., Mueller-Hill B.;
RT   "The sequence of the two extra exons in rat preA4.";
RL   Nucleic Acids Res. 17:2130-2130(1989).
RN   [3]
RP   SEQUENCE OF 720-730, AND MASS SPECTROMETRY.
RX   MEDLINE=21443797; PubMed=11483588;
RA   Gu Y., Misonou H., Sato T., Dohmae N., Takio K., Ihara Y.;
RT   "Distinct intramembrane cleavage of the beta-amyloid precursor protein
RT   family resembling gamma-secretase-like cleavage of Notch.";
RL   J. Biol. Chem. 276:35235-35238(2001).
RN   [4]
RP   ALTERNATIVE SPLICING.
RX   MEDLINE=96187032; PubMed=8624099;
RA   Sandbrink R., Masters C.L., Beyreuther K.;
RT   "APP gene family. Alternative splicing generates functionally related
RT   isoforms.";
RL   Ann. N.Y. Acad. Sci. 777:281-287(1996).
RN   [5]
RP   TISSUE SPECIFICITY OF APPICAN.
RX   MEDLINE=95263526; PubMed=7744833;
RA   Shioi J., Pangalos M.N., Ripellino J.A., Vassilacopoulou D.,
RA   Mytilineou C., Margolis R.U., Robakis N.K.;
RT   "The Alzheimer amyloid precursor proteoglycan (appican) is present in
RT   brain and is produced by astrocytes but not by neurons in primary
RT   neural cultures.";
RL   J. Biol. Chem. 270:11839-11844(1995).
RN   [6]
RP   TISSUE SPECIFICITY OF ISOFORMS.
RX   MEDLINE=97150061; PubMed=8996834;
RA   Sandbrink R., Monning U., Masters C.L., Beyreuther K.;
RT   "Expression of the APP gene family in brain cells, brain development
RT   and aging.";
RL   Gerontology 43:119-131(1997).
RN   [7]
RP   INTERACTION WITH DDB1, AND MUTAGENESIS OF TYR-757; ASN-759 AND
RP   TYR-762.
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RX   MEDLINE=99127916; PubMed=9930726;
RA   Watanabe T., Sukegawa J., Tomita S., Iijima K.-I., Oguchi S.,
RA   Suzuki T., Nairn A.C., Greengard P.;
RT   "A 127-kDa protein (UV-DDB) binds to the cytoplasmic domain of the
RT   Alzheimer's amyloid precursor protein.";
RL   J. Neurochem. 72:549-556(1999).
RN   [8]
RP   INTERACTION WITH GNAO1, AND MUTAGENESIS OF 732-HIS-HIS-733.
RX   MEDLINE=99162676; PubMed=10024358;
RA   Brouillet E., Trembleau A., Galanaud D., Volovitch M., Bouillot C.,
RA   Valenza C., Prochiantz A., Allinquant B.;
RT   "The amyloid precursor protein interacts with Go heterotrimeric
RT   protein within a cell compartment specialized in signal
RT   transduction.";
RL   J. Neurosci. 19:1717-1727(1999).
RN   [9]
RP   CHARACTERISTICS OF APPICAN, AND MUTAGENESIS OF SER-656.
RX   MEDLINE=95256193; PubMed=7737970;
RA   Pangalos M.N., Efthimiopoulos S., Shioi J., Robakis N.K.;
RT   "The chondroitin sulfate attachment site of appican is formed by
RT   splicing out exon 15 of the amyloid precursor gene.";
RL   J. Biol. Chem. 270:10388-10391(1995).
RN   [10]
RP   BETA-AMYLOID METAL-BINDING.
RX   MEDLINE=99316162; PubMed=10386999;
RA   Huang X., Atwood C.S., Hartshorn M.A., Multhaup G., Goldstein L.E.,
RA   Scarpa R.C., Cuajungco M.P., Gray D.N., Lim J., Moir R.D., Tanzi R.E.,
RA   Bush A.I.;
RT   "The A beta peptide of Alzheimer's disease directly produces hydrogen
RT   peroxide through metal ion reduction.";
RL   Biochemistry 38:7609-7616(1999).
RN   [11]
RP   BETA-AMYLOID ZINC BINDING.
RX   MEDLINE=99343552; PubMed=10413512;
RA   Liu S.T., Howlett G., Barrow C.J.;
RT   "Histidine-13 is a crucial residue in the zinc ion-induced aggregation
RT   of the A beta peptide of Alzheimer's disease.";
RL   Biochemistry 38:9373-9378(1999).
RN   [12]
RP   IMPORTANCE OF GLY-704 IN FREE RADICAL PROPAGATION, AND MUTAGENESIS OF
RP   GLY-704.
RX   MEDLINE=21956095; PubMed=11959460;
RA   Kanski J., Varadarajan S., Aksenova M., Butterfield D.A.;
RT   "Role of glycine-33 and methionine-35 in Alzheimer's amyloid beta-
RT   peptide 1-42-associated oxidative stress and neurotoxicity.";
RL   Biochim. Biophys. Acta 1586:190-198(2001).
RN   [13]
RP   PHOSPHORYLATION.
RX   MEDLINE=97239592; PubMed=9085254;
RA   Oishi M., Nairn A.C., Czernik A.J., Lim G.S., Isohara T., Gandy S.E.,
RA   Greengard P., Suzuki T.;
RT   "The cytoplasmic domain of Alzheimer's amyloid precursor protein is
RT   phosphorylated at Thr654, Ser655, and Thr668 in adult rat brain and
RT   cultured cells.";
RL   Mol. Med. 3:111-123(1997).
RN   [14]
RP   PHOSPHORYLATION ON SER-730.
RX   MEDLINE=99262094; PubMed=10329382;
RA   Isohara T., Horiuchi A., Watanabe T., Ando K., Czernik A.J., Uno I.,
RA   Greengard P., Nairn A.C., Suzuki T.;
RT   "Phosphorylation of the cytoplasmic domain of Alzheimer's beta-amyloid
RT   precursor protein at Ser655 by a novel protein kinase.";
RL   Biochem. Biophys. Res. Commun. 258:300-305(1999).
RN   [15]
RP   PHOSPHORYLATION, INDUCTION, SUBCELLULAR LOCATION, AND MUTAGENESIS OF
RP   THR-743.
RX   MEDLINE=99274744; PubMed=10341243;
RA   Ando K., Oishi M., Takeda S., Iijima K.-I., Isohara T., Nairn A.C.,
RA   Kirino Y., Greengard P., Suzuki T.;
RT   "Role of phosphorylation of Alzheimer's amyloid precursor protein
RT   during neuronal differentiation.";
RL   J. Neurosci. 19:4421-4427(1999).
RN   [16]
RP   PHOSPHORYLATION ON THR-743.
RX   MEDLINE=20396183; PubMed=10936190;
RA   Iijima K.-I., Ando K., Takeda S., Satoh Y., Seki T., Itohara S.,
RA   Greengard P., Kirino Y., Nairn A.C., Suzuki T.;
RT   "Neuron-specific phosphorylation of Alzheimer's beta-amyloid precursor
RT   protein by cyclin-dependent kinase 5.";
RL   J. Neurochem. 75:1085-1091(2000).
RN   [17]
RP   CARBOHYDRATE STRUCTURE OF APPICAN.
RX   MEDLINE=21463085; PubMed=11479316;
RA   Tsuchida K., Shioi J., Yamada S., Boghosian G., Wu A., Cai H.,
RA   Sugahara K., Robakis N.K.;
RT   "Appican, the proteoglycan form of the amyloid precursor protein,
RT   contains chondroitin sulfate E in the repeating disaccharide region
RT   and 4-O-sulfated galactose in the linkage region.";
RL   J. Biol. Chem. 276:37155-37160(2001).
CC   -!- FUNCTION: Functions as a cell surface receptor and performs
CC       physiological functions on the surface of neurons relevant to
CC       neurite growth, neuronal adhesion and axonogenesis. Involved in
CC       cell mobility and transcription regulation through protein-protein
CC       interactions (By similarity). Can promote transcription activation
CC       through binding to APBB1/Tip60 and inhibit Notch signaling through
CC       interaction with Numb (By similarity). Couples to apoptosis-
CC       inducing pathways such as those mediated by G(O) and JIP. Inhibits
CC       G(O) alpha ATPase activity. Acts as a kinesin I membrane receptor,
CC       mediating the axonal transport of beta-secretase and presenilin 1
CC       (By similarity). May be involved in copper homeostasis/oxidative
CC       stress through copper ion reduction. Can regulate neurite
CC       outgrowth through binding to components of the extracellular
CC       matrix such as heparin and collagen I and IV (By similarity). The
CC       splice isoforms that contain the BPTI domain possess protease
CC       inhibitor activity (By similarity).
CC   -!- FUNCTION: Beta-amyloid peptides are lipophilic metal chelators
CC       with metal-reducing activity. Bind transient metals such as
CC       copper, zinc and iron. Rat and mouse beta-amyloid peptides bind
CC       only weakly transient metals and have little reducing activity due
CC       to substitutions of transient metal chelating residues. Beta-APP42
CC       may activate mononuclear phagocytes in the brain and elicit
CC       inflammatory responses. Promotes both tau aggregation and TPK II-
CC       mediated phosphorylation (By similarity).
CC   -!- FUNCTION: Appicans elicit adhesion of neural cells to the
CC       extracellular matrix and may regulate neurite outgrowth in the
CC       brain.
CC   -!- FUNCTION: The gamma-CTF peptides as well as the caspase-cleaved
CC       peptides, including C31, are potent enhancers of neuronal
CC       apoptosis (By similarity).
CC   -!- SUBUNIT: Binds, via its C-terminal, to the PID domain of several
CC       cytoplasmic proteins, including APBB family members, the APBA
CC       family, MAPK8IP1, SHC1 and Numb and Dab1 (By similarity). Binding
CC       to Dab1 inhibits its serine phosphorylation (By similarity). Also
CC       interacts with GPCR-like protein BPP, FPRL1, APPBP1, IB1, KNS2
CC       (via its TPR domains), APPBP2 (via BaSS) (By similarity) and DDB1.
CC       In vitro, it binds MAPT via the MT-binding domains (By
CC       similarity). Associates with microtubules in the presence of ATP
CC       and in a kinesin-dependent manner (By similarity). Interacts,
CC       through a C-terminal domain, with GNAO1. Amyloid beta-42 binds
CC       CHRNA7 in hippocampal neurons (By similarity). Beta-amyloid
CC       associates with HADH2 (By similarity).
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein. Cell surface
CC       protein that rapidly becomes internalized via clathrin-coated
CC       pits. During maturation, the immature APP (N-glycosylated in the

  Query Match             91.5%;  Score 321;  DB 1;  Length 770;
  Best Local Similarity   94.9%;  Pred. No. 1.6e-30;
  Matches   56;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 EVVREVCSEQAETGPCRAAIYHWYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMAVCGS 59
              |||||||||||||||||||| | ||||||||||||||||||||||||||||||||||||
Db        285 EVVREVCSEQAETGPCRAMISRWYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMAVCGS 343


RESULT 6
A4_CAVPO
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ID   A4_CAVPO        STANDARD;      PRT;   770 AA.
AC   Q60495; Q60496;
DT   10-OCT-2003 (Rel. 42, Created)
DT   10-OCT-2003 (Rel. 42, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Amyloid beta A4 protein precursor (APP) (ABPP) (Alzheimer's disease
DE   amyloid protein homolog) [Contains: Soluble APP-alpha (S-APP-alpha);
DE   Soluble APP-beta (S-APP-beta); CTF-alpha; CTF-beta; Beta-amyloid
DE   protein 42 (Beta-APP42); Beta-amyloid protein 40 (Beta-APP40); P3(42);
DE   P3(40); CTF(59) (Gamma-secretase C-terminal fragment 59); Gamma-
DE   CTF(57) (Gamma-secretase C-terminal fragment 57); C31].
GN   APP.
OS   Cavia porcellus (Guinea pig).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
OX   NCBI_TaxID=10141;
RN   [1]
RP   SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
RC   TISSUE=Brain, and Liver;
RX   MEDLINE=97236426; PubMed=9116031;
RA   Beck M., Mueller D., Bigl V.;
RT   "Amyloid precursor protein in Guinea pigs - complete cDNA sequence and
RT   alternative splicing.";
RL   Biochim. Biophys. Acta 1351:17-21(1997).
RN   [2]
RP   INTERACTION OF BETA-APP40 WITH APOE.
RX   MEDLINE=98007700; PubMed=9349544;
RA   Martel C.L., Mackic J.B., Matsubara E., Governale S., Miguel C.,
RA   Miao W., McComb J.G., Frangione B., Ghiso J., Zlokovic B.V.;
RT   "Isoform-specific effects of apolipoproteins E2, E3, and E4 on
RT   cerebral capillary sequestration and blood-brain barrier transport of
RT   circulating Alzheimer's amyloid beta.";
RL   J. Neurochem. 69:1995-2004(1997).
RN   [3]
RP   PROCESSING.
RX   MEDLINE=20084499; PubMed=10619481;
RA   Beck M., Brueckner M.K., Holzer M., Kaap S., Pannicke T., Arendt T.,
RA   Bigl V.;
RT   "Guinea-pig primary cell cultures provide a model to study expression
RT   and amyloidogenic processing of endogenous amyloid precursor
RT   protein.";
RL   Neuroscience 95:243-254(2000).
RN   [4]
RP   GAMMA-SECRETASE PROCESSING.
RX   MEDLINE=20576391; PubMed=11035007;
RA   Pinnix I., Musunuru U., Tun H., Sridharan A., Golde T., Eckman C.,
RA   Ziani-Cherif C., Onstead L., Sambamurti K.;
RT   "A novel gamma -secretase assay based on detection of the putative
RT   C-terminal fragment-gamma of amyloid beta protein precursor.";
RL   J. Biol. Chem. 276:481-487(2001).
CC   -!- FUNCTION: Functions as a cell surface receptor and performs
CC       physiological functions on the surface of neurons relevant to
CC       neurite growth, neuronal adhesion and axonogenesis. Involved in
CC       cell mobility and transcription regulation through protein-protein
CC       interactions (By similarity). Can promote transcription activation
CC       through binding to APBB1/Tip60 and inhibit Notch signaling through
CC       interaction with Numb (By similarity). Couples to apoptosis-
CC       inducing pathways such as those mediated by G(O) and JIP (By
CC       similarity). Inhibits G(O) alpha ATPase activity (By similarity).
CC       Acts as a kinesin I membrane receptor, mediating the axonal
CC       transport of beta-secretase and presenilin 1 (By similarity). May
CC       be involved in copper homeostasis/oxidative stress through copper
CC       ion reduction (By similarity). In vitro, copper-metallated APP
CC       induces neuronal death directly or is potentiated through Cu(II)-
CC       mediated low-density lipoprotein oxidation (By similarity). Can
CC       regulate neurite outgrowth through binding to components of the
CC       extracellular matrix such as heparin and collagen I and IV (By
CC       similarity). The splice isoforms that contain the BPTI domain
CC       possess protease inhibitor activity (By similarity).
CC   -!- FUNCTION: Beta-amyloid peptides are lipophilic metal chelators
CC       with metal-reducing activity. Bind transient metals such as
CC       copper, zinc and iron. Beta-amyloid peptides bind to lipoproteins
CC       and apoliproteins E and J in the CSF and to HDL particles in
CC       plasma, inhibiting metal-catalyzed oxidation of lipoproteins.
CC   -!- FUNCTION: Appicans elicit adhesion of neural cells to the
CC       extracellular matrix and may regulate neurite outgrowth in the
CC       brain (By similarity).
CC   -!- FUNCTION: The gamma-CTF peptides as well as the caspase-cleaved
CC       peptides, including C31, are potent enhancers of neuronal
CC       apoptosis (By similarity).
CC   -!- SUBUNIT: Binds, via its C-terminal, to the PID domain of several
CC       cytoplasmic proteins, including APBB family members, the APBA
CC       family, MAPK8IP1, SHC1 and Numb and Dab1 (By similarity). Also
CC       interacts with GPCR-like protein BPP, FPRL1, APPBP1, IB1, KNS2
CC       (via its TPR domains), APPBP2 (via BaSS) and DDB1 (By similarity).
CC       Associates with microtubules in the presence of ATP and in a
CC       kinesin-dependent manner (By similarity). Soluble Abeta40 binds
CC       all three isoforms of APOE, in vitro and in vivo. When lipidated,
CC       ApoE3 appears to be the preferred amyloid binding isoform, while
CC       the apoE4 isoform-beta-APP40 complex is capable of being
CC       transported across the blood-brain barrier.
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein. Cell surface
CC       protein that rapidly becomes internalized via clathrin-coated pits
CC       (By similarity). During maturation, the immature APP (N-
CC       glycosylated in the endoplasmic reticulum) moves to the Golgi
CC       complex where complete maturation occurs (O-glycosylated and
CC       sulfated) (By similarity). After alpha-secretase cleavage, soluble
CC       APP is released into the extracellular space and the C-terminal is
CC       internalized to endosomes and lysosomes (By similarity). Some APP
CC       accumulates in secretory transport vesicles leaving the late Golgi
CC       compartment and returns to the cell surface (By similarity). APP
CC       sorts to the basolateral surface in epithelial cells (By
CC       similatity).
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=2;
CC         Comment=Additional isoforms, missing exons 7,8 and 15, seem to
CC         exist. The L-isoforms, missing exon 15, are referred to as
CC         appicans;
CC       Name=APP770;
CC         IsoId=Q60495-1; Sequence=Displayed;
CC       Name=APP695;
CC         IsoId=Q60495-2; Sequence=VSP_007221, VSP_007222;
CC   -!- TISSUE SPECIFICITY: Isoform APP695 is the major isoform found in
CC       brain. The longer isoforms containing the BPTI domain are
CC       predominantly expressed in peripheral organs such as muscle and
CC       liver.
CC   -!- INDUCTION: Increased levels during neuronal differentiation.
CC   -!- DOMAIN: The basolateral sorting signal (BaSS) is required for
CC       sorting of membrane proteins to the basolateral surface of
CC       epithelial cells.
CC   -!- DOMAIN: The NPXY sequence motif found in many tyrosine-
CC       phosphorylated proteins is required for the specific binding of
CC       the PID domain. However additional amino acids either N- or C-
CC       terminal to the NPXY motif are often required for complete
CC       interaction. The PID domain-containing proteins which bind APP
CC       require the YENPTY motif for full interaction. These interactions
CC       are independent of phosphorylation on the terminal tyrosine
CC       residue (By similarity). The NPXY site is also involved in
CC       clathrin-mediated endocytosis.
CC   -!- PTM: Proteolytically processed under normal cellular conditions.
CC       Cleavage by alpha-secretase or alternatively by beta-secretase
CC       leads to generation and extracellular release of soluble APP
CC       peptides, S-APP-alpha and S-APP-beta, respectively, and the
CC       retention of corresponding membrane-anchored C-terminal fragments,
CC       CTF-alpha and CTF-beta. Subsequent processing of CTF-alpha by
CC       gamma-secretase yields P3 peptides. This is the major secretory
CC       pathway and is nonamyloidogenic. Alternatively,
CC       presenilin/nicastrin-mediated gamma-secretase processing of CTF-
CC       beta releases the amyloid beta proteins, amyloid-beta 40 (Abeta40)
CC       and amyloid-beta 42 (Abeta42), major components of amyloid
CC       plaques, and the corresponding cytotoxic C-terminal fragments
CC       (CTFs).
CC   -!- PTM: Proteolytically cleaved by caspase-3 during neuronal
CC       apoptosis (By similarity).
CC   -!- PTM: N- and O-glycosylated. O-linkage of chondroitin sulfate to
CC       the L-APP isoforms produces the APP proteoglycan core proteins,
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CC       the appicans (By similarity).
CC   -!- PTM: Phosphorylation in the C-terminal on tyrosine, threonine and
CC       serine residues is neuron-specific (By similarity).
CC       Phosphorylation can affect APP processing, neuronal
CC       differentiation and interaction with other proteins.
CC   -!- PTM: Extracellular binding and reduction of copper, results in a
CC       corresponding oxidation of Cys-144 and Cys-158, and the formation
CC       of a disulfide bond (By similarity).
CC   -!- MISCELLANEOUS: Chelation of metal ions, notably copper, iron and
CC       zinc, can induce histidine-bridging between beta-amyloid molecules
CC       resulting in beta-amyloid-metal aggregates.
CC   -!- SIMILARITY: Belongs to the APP family.
CC   -!- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
CC   ----------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC   use by non-profit institutions as long as its content is in no way
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CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; X97631; CAA66230.1; -.
DR   EMBL; X99198; CAA67589.1; -.
DR   HSSP; P05067; 1BA4.
DR   InterPro; IPR008155; A4_APP.
DR   InterPro; IPR008154; A4_extra.
DR   InterPro; IPR002223; Kunitz_BPTI.
DR   Pfam; PF00014; Kunitz_BPTI; 1.
DR   PRINTS; PR00203; AMYLOIDA4.
DR   PRINTS; PR00759; BASICPTASE.
DR   ProDom; PD000222; Kunitz_BPTI; 1.
DR   SMART; SM00006; A4_EXTRA; 1.
DR   SMART; SM00131; KU; 1.
DR   PROSITE; PS00319; A4_EXTRA; 1.
DR   PROSITE; PS00320; A4_INTRA; 1.
DR   PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR   PROSITE; PS50279; BPTI_KUNITZ_2; 1.
KW   Apoptosis; Endocytosis; Cell adhesion; Serine protease inhibitor;
KW   Coated pits; Neurone; Heparin-binding; Metal-binding; Copper; Iron;
KW   Zinc; Signal; Transmembrane; Glycoprotein; Phosphorylation;
KW   Proteoglycan; Alternative splicing; Amyloid.
FT   SIGNAL        1     17       BY SIMILARITY.
FT   CHAIN        18    770       AMYLOID BETA A4 PROTEIN.
FT   CHAIN        18    687       SOLUBLE APP-ALPHA (BY SIMILARITY).
FT   CHAIN        18    671       SOLUBLE APP-BETA (BY SIMILARITY).
FT   CHAIN       672    770       CTF-ALPHA (BY SIMILARITY).
FT   CHAIN       672    713       BETA-AMYLOID PROTEIN 42 (BY SIMILARITY).
FT   CHAIN       672    711       BETA-AMYLOID PROTEIN 40 (BY SIMILARITY).
FT   CHAIN       688    770       CTF-BETA (BY SIMILARITY).
FT   CHAIN       688    713       P3(42) (BY SIMILARITY).
FT   CHAIN       688    711       P3(40) (BY SIMILARITY).
FT   CHAIN       712    770       GAMMA-CTF(59) (BY SIMILARITY).
FT   CHAIN       714    770       GAMMA-CTF(57) (BY SIMILARITY).

  Query Match             90.9%;  Score 319;  DB 1;  Length 770;
  Best Local Similarity   90.2%;  Pred. No. 2.7e-30;
  Matches   55;  Conservative    2;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 EVVREVCSEQAETGPCRAAIYHWYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMAVCGSA 60
              |||||||||||||||||: |  ||||||||||||||||||||||||||||||||||||
Db        285 EVVREVCSEQAETGPCRSMISRWYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMAVCGSV 344

Qy         61 I 61
              :
Db        345 M 345


RESULT 7
A4_MOUSE
ID   A4_MOUSE       STANDARD;      PRT;   770 AA.
AC   P12023; P97487; P97942; Q99K32;
DT   01-OCT-1989 (Rel. 12, Created)
DT   10-OCT-2003 (Rel. 42, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Amyloid beta A4 protein precursor (APP) (ABPP) (Alzheimer's disease
DE   amyloid protein homolog) (Amyloidogenic glycoprotein) (AG) [Contains:
DE   Soluble APP-alpha (S-APP-alpha); Soluble APP-beta (S-APP-beta); C99
DE   (APP-C99); Beta-amyloid protein 42 (Beta-APP42); Beta-amyloid protein
DE   40 (Beta-APP40); C83; P3(42); P3(40); Gamma-CTF(59) (Gamma-secretase
DE   C-terminal fragment 59) (Amyloid intracellular domain 59) (AID(59))
DE   (APP-C59); Gamma-CTF(57) (Gamma-secretase C-terminal fragment 57)
DE   (Amyloid intracellular domain 57) (AID(57)) (APP-C57); Gamma-CTF(50)
DE   (Gamma-secretase C-terminal fragment 50) (Amyloid intracellular domain
DE   50) (AID(50)); C31].
GN   APP.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A. (ISOFORM APP695).
RC   TISSUE=Brain;
RX   MEDLINE=88106489; PubMed=3322280;
RA   Yamada T., Sasaki H., Furuya H., Miyata T., Goto I., Sakaki Y.;
RT   "Complementary DNA for the mouse homolog of the human amyloid beta
RT   protein precursor.";
RL   Biochem. Biophys. Res. Commun. 149:665-671(1987).
RN   [2]
RP   REVISIONS.
RA   Yamada T.;
RL   Submitted (MAR-1988) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   SEQUENCE FROM N.A. (ISOFORM APP695).
RC   STRAIN=BALB/c; TISSUE=Brain;
RX   MEDLINE=92096458; PubMed=1756177;
RA   de Strooper B., van Leuven F., van den Berghe H.;
RT   "The amyloid beta protein precursor or proteinase nexin II from mouse
RT   is closer related to its human homolog than previously reported.";
RL   Biochim. Biophys. Acta 1129:141-143(1991).
RN   [4]
RP   SEQUENCE FROM N.A. (ISOFORM APP695).
RC   STRAIN=SAMP8; TISSUE=Hippocampus;
RX   MEDLINE=21130647; PubMed=11235921;
RA   Kumar V.B., Vyas K., Franko M., Choudhary V., Buddhiraju C.,
RA   Alvarez J., Morley J.E.;
RT   "Molecular cloning, expression, and regulation of hippocampal amyloid
RT   precursor protein of senescence accelerated mouse (SAMP8).";
RL   Biochem. Cell Biol. 79:57-67(2001).
RN   [5]
RP   SEQUENCE OF 1-19 FROM N.A.
RX   MEDLINE=92209998; PubMed=1555768;
RA   Izumi R., Yamada T., Yoshikai S.I., Sasaki H., Hattori M.,
RA   Sakai Y.;
RT   "Positive and negative regulatory elements for the expression of the
RT   Alzheimer's disease amyloid precursor-encoding gene in mouse.";
RL   Gene 112:189-195(1992).
RN   [6]
RP   PARTIAL SEQUENCE FROM N.A. (ISOFORM APP770).
RC   TISSUE=Breast tumor;
RX   MEDLINE=22388257; PubMed=12477932;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
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RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [7]
RP   SEQUENCE OF 281-380 FROM N.A., AND ALTERNATIVE SPLICING.
RC   TISSUE=Brain, and Kidney;
RX   MEDLINE=89149813; PubMed=2493250;
RA   Yamada T., Sasaki H., Dohura K., Goto I., Sakaki Y.;
RT   "Structure and expression of the alternatively-spliced forms of mRNA
RT   for the mouse homolog of Alzheimer's disease amyloid beta protein
RT   precursor.";
RL   Biochem. Biophys. Res. Commun. 158:906-912(1989).
RN   [8]
RP   SEQUENCE OF 289-364 FROM N.A.
RC   STRAIN=CD-1; TISSUE=Placenta;
RX   MEDLINE=89345111; PubMed=2569710;
RA   Fukuchi K., Martin G.M., Deeb S.S.;
RT   "Sequence of the protease inhibitor domain of the A4 amyloid protein
RT   precursor of Mus domesticus.";
RL   Nucleic Acids Res. 17:5396-5396(1989).
RN   [9]
RP   SEQUENCE OF 656-737 FROM N.A.
RC   STRAIN=129/Sv;
RA   Wragg M.A., Busfield F., Duff K., Korenblat K., Capecchi M.,
RA   Loring J.F., Goate A.M.;
RT   "Introduction of six mutations into the mouse genome using 'Hit and
RT   Run' gene-targeting: introduction of familial Alzheimer's disease
RT   mutations into the mouse amyloid precursor protein gene and
RT   humanization of the A-beta fragment.";
RL   Submitted (DEC-1996) to the EMBL/GenBank/DDBJ databases.
RN   [10]
RP   TISSUE SPECIFICITY OF ALTERNATIVE SPLICED FORMS.
RX   MEDLINE=93287808; PubMed=8510506;
RA   Sola C., Mengod G., Ghetti B., Palacios J.M., Triarhou L.C.;
RT   "Regional distribution of the alternatively spliced isoforms of beta
RT   APP RNA transcript in the brain of normal, heterozygous and
RT   homozygous weaver mutant mice as revealed by in situ hybridization
RT   histochemistry.";
RL   Brain Res. Mol. Brain Res. 17:340-346(1993).
RN   [11]
RP   INTERACTION WITH KNS2.
RX   MEDLINE=21010507; PubMed=11144355;
RA   Kamal A., Stokin G.B., Yang Z., Xia C.-H., Goldstein L.S.;
RT   "Axonal transport of amyloid precursor protein is mediated by direct
RT   binding to the kinesin light chain subunit of kinesin-I.";
RL   Neuron 28:449-459(2000).
RN   [12]
RP   C-TERMINAL PROTEIN-PROTEIN INTERACTIONS, AND MUTAGENESIS OF TYR-728;
RP   THR-743; TYR-757; ASN-759 AND TYR-762.
RX   MEDLINE=21408156; PubMed=11517249;
RA   Matsuda S., Yasukawa T., Homma Y., Ito Y., Niikura T., Hiraki T.,
RA   Hirai S., Ohno S., Kita Y., Kawasumi M., Kouyama K., Yamamoto T.,
RA   Kyriakis J.M., Nishimoto I.;
RT   "C-jun N-terminal kinase (JNK)-interacting protein-1b/islet-brain-1
RT   scaffolds Alzheimer's amyloid precursor protein with JNK.";
RL   J. Neurosci. 21:6597-6607(2001).
RN   [13]
RP   INTERACTION WITH MAPK8IP1, AND PHOSPHORYLATION.
RX   MEDLINE=22028091; PubMed=11912189;
RA   Taru H., Iijima K.-I., Hase M., Kirino Y., Yagi Y., Suzuki T.;
RT   "Interaction of Alzheimer's beta-amyloid precursor family proteins
RT   with scaffold proteins of the JNK signaling cascade.";
RL   J. Biol. Chem. 277:20070-20078(2002).
RN   [14]
RP   INTERACTION OF CTF PEPTIDES WITH NUMB.
RX   MEDLINE=22008109; PubMed=12011466;
RA   Roncarati R., Sestan N., Scheinfeld M.H., Berechid B.E., Lopez P.A.,
RA   Meucci O., McGlade J.C., Rakic P., D'Adamio L.;
RT   "The gamma-secretase-generated intracellular domain of beta-amyloid
RT   precursor protein binds Numb and inhibits Notch signaling.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:7102-7107(2002).
RN   [15]
RP   GAMMA-SECRETASE PROCESSING, AND INTERACTION WITH APBB1.
RX   MEDLINE=21437805; PubMed=11553691;
RA   Cupers P., Orlans I., Craessaerts K., Annaert W., De Strooper B.;
RT   "The amyloid precursor protein (APP)-cytoplasmic fragment generated by
RT   gamma-secretase is rapidly degraded but distributes partially in a
RT   nuclear fraction of neurones in culture.";
RL   J. Neurochem. 78:1168-1178(2001).
CC   -!- FUNCTION: Functions as a cell surface receptor and performs
CC       physiological functions on the surface of neurons relevant to
CC       neurite growth, neuronal adhesion and axonogenesis. Involved in
CC       cell mobility and transcription regulation through protein-protein
CC       interactions. Can promote transcription activation through binding
CC       to APBB1/Tip60 and inhibit Notch signaling through interaction
CC       with Numb. Couples to apoptosis-inducing pathways such as those
CC       mediated by G(O) and JIP. Inhibits G(0) alpha ATPase activity (By
CC       similarity). Acts as a kinesin I membrane receptor, mediating the
CC       axonal transport of beta-secretase and presenilin 1. May be
CC       involved in copper homeostasis/oxidative stress through copper ion
CC       reduction. Can regulate neurite outgrowth through binding to
CC       components of the extracellular matrix such as heparin and
CC       collagen I and IV (By similarity). The splice isoforms that
CC       contain the BPTI domain possess protease inhibitor activity (By
CC       similarity).
CC   -!- FUNCTION: Beta-amyloid peptides are lipophilic metal chelators
CC       with metal-reducing activity. Bind transient metals such as
CC       copper, zinc and iron. Rat and mouse beta-amyloid peptides bind
CC       only weakly transient metals and have little reducing activity due
CC       to substitutions of transient metal chelating residues. Beta-APP42
CC       may activate mononuclear phagocytes in the brain and elicit
CC       inflammatory responses. Promotes both tau aggregation and TPK II-
CC       mediated phosphorylation (By similarity).
CC   -!- FUNCTION: The gamma-CTF peptides as well as the caspase-cleaved
CC       peptides, including C31, are potent enhancers of neuronal
CC       apoptosis.
CC   -!- SUBUNIT: Binds, via its C-terminal, to the PID domain of several
CC       cytoplasmic proteins, including APBB family members, the APBA
CC       family, MAPK8IP1, SHC1, Numb and Dab1. Binding to Dab1 inhibits
CC       its serine phosphorylation. Also interacts with GPCR-like protein
CC       BPP, FPRL1, APPBP1, IB1, KNS2 (via its TPR domains), APPBP2 (via
CC       BaSS) and DDB1 (By similarity). In vitro, it binds MAPT via the
CC       MT-binding domains (By similarity). Associates with microtubules
CC       in the presence of ATP and in a kinesin-dependent manner (By
CC       similarity). Interacts, through a C-terminal domain, with GNAO1
CC       (By similarity). Amyloid beta-42 binds CHRNA7 in hippocampal
CC       neurons (By similarity). Beta-amyloid associates with HADH2 (By
CC       similarity).
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein. Cell surface
CC       protein that rapidly becomes internalized via clathrin-coated
CC       pits. During maturation, the immature APP (N-glycosylated in the
CC       endoplasmic reticulum) moves to the Golgi complex where complete

  Query Match             90.3%;  Score 317;  DB 1;  Length 770;
  Best Local Similarity   93.2%;  Pred. No. 4.7e-30;
  Matches   55;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 EVVREVCSEQAETGPCRAAIYHWYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMAVCGS 59
              ||||||||||||||||||| | |||||||||| |||||||||||||||||||||||||||
Db        285 EVVREVCSEQAETGPCRAMISRWYFDVTEGKCVPFFYGGCGGNRNNFDTEEYCMAVCGS 343


RESULT 8
A4_MACMU
ID   A4_MACMU       STANDARD;      PRT;    76 AA.
AC   P29216;
DT   01-DEC-1992 (Rel. 24, Created)
DT   01-DEC-1992 (Rel. 24, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Alzheimer's disease amyloid A4 protein (Fragment).
GN   APP.
OS   Macaca mulatta (Rhesus macaque).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
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OC   Cercopithecinae; Macaca.
OX   NCBI_TaxID=9544;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RX   MEDLINE=90180499; PubMed=2106906;
RA   Koo E.H., Sisodia S.S., Cork L.C., Unterbeck A., Bayney R.M.,
RA   Price D.L.;
RT   "Differential expression of amyloid precursor protein mRNAs in cases
RT   of Alzheimer's disease and in aged nonhuman primates.";
RL   Neuron 4:97-104(1990).
CC   -!- FUNCTION: Functional neuronal receptor which couples to
CC       intracellular signaling pathway through the GTP-binding protein
CC       G(O) (By similarity).
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=5;
CC         Comment=Experimental confirmation may be lacking for some
CC         isoforms;
CC       Name=APP(770);
CC         IsoId=P29216-1; Sequence=Displayed;
CC       Name=APP(395);
CC         IsoId=P29216-2; Sequence=Not described;
CC       Name=APP(563);
CC         IsoId=P29216-3; Sequence=Not described;
CC       Name=APP(695);
CC         IsoId=P29216-4; Sequence=Not described;
CC       Name=APP(751);
CC         IsoId=P29216-5; Sequence=Not described;
CC   -!- SIMILARITY: Belongs to the APP family.
CC   -!- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
CC   ----------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; X15985; CAA34116.1; -.
DR   PIR; S06678; S06678.
DR   HSSP; P05067; 1AAP.
DR   InterPro; IPR008155; A4_APP.
DR   InterPro; IPR002223; Kunitz_BPTI.
DR   Pfam; PF00014; Kunitz_BPTI; 1.
DR   PRINTS; PR00759; BASICPTASE.
DR   ProDom; PD000222; Kunitz_BPTI; 1.
DR   SMART; SM00131; KU; 1.
DR   PROSITE; PS00319; A4_EXTRA; PARTIAL.
DR   PROSITE; PS00320; A4_INTRA; PARTIAL.
DR   PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR   PROSITE; PS50279; BPTI_KUNITZ_2; 1.
KW   Glycoprotein; Amyloid; Neurone; Alternative splicing;
KW   Serine protease inhibitor.
FT   NON_TER       1      1
FT   DOMAIN        1     76       BPTI/KUNITZ INHIBITOR.
FT   ACT_SITE     13     14       REACTIVE BOND.
FT   DISULFID      3     53       BY SIMILARITY.
FT   DISULFID     12     36       BY SIMILARITY.
FT   DISULFID     28     49       BY SIMILARITY.
FT   NON_TER      76     76
SQ   SEQUENCE   76 AA;  8527 MW;  492BF3069AB082A1 CRC64;

  Query Match             86.6%;  Score 304;  DB 1;  Length 76;
  Best Local Similarity   91.2%;  Pred. No. 1.7e-29;
  Matches   52;  Conservative    1;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          5 EVCSEQAETGPCRAAIYHWYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMAVCGSAI 61
              ||||||||||||||| |  ||||||||||||||||||||||||||||||||||| :
Db          1 EVCSEQAETGPCRAMISRWYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMAVCGSVM 57
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RESULT 9
APP2_HUMAN
ID   APP2_HUMAN     STANDARD;      PRT;   763 AA.
AC   Q06481;
DT   01-JUN-1994 (Rel. 29, Created)
DT   01-OCT-1996 (Rel. 34, Last sequence update)
DT   15-MAR-2004 (Rel. 43, Last annotation update)
DE   Amyloid-like protein 2 precursor (Amyloid protein homolog) (APPH)
DE   (CDEI-box binding protein) (CDEBP).
GN   APLP2 OR APPL2.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Placenta;
RX   MEDLINE=93250009; PubMed=8485127;
RA   Sprecher C.A., Grant F.J., Grimm G., O'Hara P.J., Norris F.,
RA   Norris K., Foster D.C.;
RT   "Molecular cloning of the cDNA for a human amyloid precursor protein
RT   homolog: evidence for a multigene family.";
RL   Biochemistry 32:4481-4486(1993).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Ovary;
RX   MEDLINE=95217334; PubMed=7702756;
RA   von der Kammer H., Hanes J., Klaudiny J., Scheit K.H.;
RT   "A human amyloid precursor-like protein is highly homologous to a
RT   mouse sequence-specific DNA-binding protein.";
RL   DNA Cell Biol. 13:1137-1143(1994).
RN   [3]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RX   MEDLINE=94035131; PubMed=8220435;
RA   Wasco W., Gurubhagavatula S., Paradis M., Romano D.M., Sisodia S.S.,
RA   Hyman B.T., Neve R.L., Tanzi R.E.;
RT   "Isolation and characterization of APLP2 encoding a homologue of the
RT   Alzheimer's associated amyloid beta protein precursor.";
RL   Nat. Genet. 5:95-99(1993).
RN   [4]
RP   SEQUENCE FROM N.A. (ISOFORM 3).
RC   TISSUE=Lung;
RX   MEDLINE=22388257; PubMed=12477932;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length
RT   human and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC   -!- FUNCTION: May play a role in the regulation of hemostasis. The
CC       soluble form may have inhibitory properties towards coagulation
CC       factors. May interact with cellular G-protein signaling pathways.
CC       May bind to the DNA 5'-GTCACATG-3'(CDEI box).
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein and nuclear
CC       (Potential).
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=3;
CC         Comment=Additional isoforms seem to exist;
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CC       Name=1;
CC         IsoId=Q06481-1; Sequence=Displayed;
CC       Name=2;
CC         IsoId=Q06481-2; Sequence=VSP_000018;
CC       Name=3;
CC         IsoId=Q06481-3; Sequence=VSP_000019;
CC   -!- TISSUE SPECIFICITY: In placenta, brain, heart, lung, liver, kidney
CC       and endothelial tissues.
CC   -!- SIMILARITY: Belongs to the APP family.
CC   -!- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; S60099; AAC60589.1; -.
DR   EMBL; L09209; AAA35526.1; -.
DR   EMBL; Z22572; CAA80295.1; -.
DR   EMBL; L27631; AAC41701.1; -.
DR   EMBL; BC000373; AAH00373.1; -.
DR   PIR; A49321; A49321.
DR   HSSP; P05067; 1MWP.
DR   Genew; HGNC:598; APLP2.
DR   MIM; 104776; -.
DR   GO; GO:0016021; C:integral to membrane; NAS.
DR   GO; GO:0005634; C:nucleus; IDA.
DR   GO; GO:0003677; F:DNA binding; NAS.
DR   GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; NAS.
DR   InterPro; IPR008155; A4_APP.
DR   InterPro; IPR008154; A4_extra.
DR   InterPro; IPR002223; Kunitz_BPTI.
DR   Pfam; PF02177; A4_EXTRA; 1.
DR   Pfam; PF00014; Kunitz_BPTI; 1.
DR   PRINTS; PR00203; AMYLOIDA4.
DR   PRINTS; PR00759; BASICPTASE.
DR   ProDom; PD000222; Kunitz_BPTI; 1.
DR   SMART; SM00006; A4_EXTRA; 1.
DR   SMART; SM00131; KU; 1.
DR   PROSITE; PS00319; A4_EXTRA; 1.
DR   PROSITE; PS00320; A4_INTRA; 1.
DR   PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR   PROSITE; PS50279; BPTI_KUNITZ_2; 1.
KW   Transmembrane; Signal; Alternative splicing; DNA-binding;
KW   Nuclear protein; Serine protease inhibitor.
FT   SIGNAL        1     29       POTENTIAL.
FT   CHAIN        30    763       AMYLOID-LIKE PROTEIN 2.
FT   DOMAIN       30    692       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    693    716       POTENTIAL.
FT   DOMAIN      717    763       CYTOPLASMIC (POTENTIAL).
FT   DOMAIN      215    280       ASP/GLU-RICH (HIGHLY ACIDIC).
FT   DOMAIN      306    364       BPTI/KUNITZ INHIBITOR.
FT   DOMAIN      215    231       POLY-GLU.
FT   ACT_SITE    320    321       REACTIVE BOND (BY SIMILARITY).
FT   DISULFID    310    360       BY SIMILARITY.
FT   DISULFID    319    343       BY SIMILARITY.
FT   DISULFID    335    356       BY SIMILARITY.
FT   VARSPLIC    308    363       Missing (in isoform 2).
FT                                /FTId=VSP_000018.
FT   VARSPLIC    613    624       Missing (in isoform 3).
FT                                /FTId=VSP_000019.
FT   CONFLICT    543    543       S -> I (IN REF. 1).
SQ   SEQUENCE   763 AA;  86955 MW;  CA3A7D6DDB8A28D0 CRC64;

  Query Match             67.8%;  Score 238;  DB 1;  Length 763;
  Best Local Similarity   64.4%;  Pred. No. 1.1e-20;
  Matches   38;  Conservative   11;  Mismatches   10;  Indels    0;  Gaps    0;

Qy          3 VREVCSEQAETGPCRAAIYHWYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMAVCGSAI 61
              |: |||::| |||||| :  ||||:::|||  | ||||||||||::|:|||||| : |

Db        306 VKAVCSQEAMTGPCRAVMPRWYFDLSKGKCVRFIYGGCGGNRNNFESEDYCMAVCKAMI 364


RESULT 10
APP2_RAT
ID   APP2_RAT       STANDARD;      PRT;   765 AA.
AC   P15943;
DT   01-APR-1990 (Rel. 14, Created)
DT   01-OCT-1996 (Rel. 34, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   Amyloid-like protein 2 precursor (Sperm membrane protein YWK-II).
GN   APLP2.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE OF 1-627 FROM N.A.
RC   STRAIN=Wistar; TISSUE=Brain, and Heart;
RX   MEDLINE=94368849; PubMed=8086458;
RA   Sandbrink R., Masters C.L., Beyreuther K.;
RT   "Complete nucleotide and deduced amino acid sequence of rat amyloid
RT   protein precursor-like protein 2 (APLP2/APPH): two amino acids length
RT   difference to human and murine homologues.";
RL   Biochim. Biophys. Acta 1219:167-170(1994).
RN   [2]
RP   SEQUENCE OF 575-765 FROM N.A.
RC   TISSUE=Testis;
RX   MEDLINE=90207205; PubMed=1690887;
RA   Yan Y.C., Bai Y., Wang L.F., Miao S.Y., Koide S.S.;
RT   "Characterization of cDNA encoding a human sperm membrane protein
RT   related to A4 amyloid protein.";
RL   Proc. Natl. Acad. Sci. U.S.A. 87:2405-2408(1990).
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=4;
CC       Name=A;
CC         IsoId=P15943-1; Sequence=Displayed;
CC       Name=B;
CC         IsoId=P15943-2; Sequence=VSP_000021;
CC       Name=C;
CC         IsoId=P15943-3; Sequence=VSP_000020;
CC       Name=D;
CC         IsoId=P15943-4; Sequence=VSP_000020, VSP_000021;
CC   -!- SIMILARITY: Belongs to the APP family.
CC   -!- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; X77934; CAA54906.1; -.
DR   EMBL; M31322; AAA42352.1; -.
DR   PIR; A35981; A35981.
DR   PIR; S42880; S42880.
DR   HSSP; P05067; 1MWP.
DR   InterPro; IPR008155; A4_APP.
DR   InterPro; IPR008154; A4_extra.
DR   InterPro; IPR002223; Kunitz_BPTI.
DR   Pfam; PF02177; A4_EXTRA; 1.
DR   Pfam; PF00014; Kunitz_BPTI; 1.
DR   PRINTS; PR00203; AMYLOIDA4.
DR   PRINTS; PR00759; BASICPTASE.
DR   ProDom; PD000222; Kunitz_BPTI; 1.
DR   SMART; SM00006; A4_EXTRA; 1.
DR   SMART; SM00131; KU; 1.
DR   PROSITE; PS00319; A4_EXTRA; 1.
DR   PROSITE; PS00320; A4_INTRA; 1.
DR   PROSITE; PS00280; BPTI_KUNITZ_1; 1.
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```
DR   PROSITE; PS50279; BPTI_KUNITZ_2; 1.
KW   Transmembrane; Alternative splicing; Serine protease inhibitor;
KW   Signal; Glycoprotein.
FT   SIGNAL        1     29       POTENTIAL.
FT   CHAIN        30    765       AMYLOID-LIKE PROTEIN 2.
FT   DOMAIN       30    695       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    696    718       POTENTIAL.
FT   DOMAIN      719    765       CYTOPLASMIC (POTENTIAL).
FT   DOMAIN      218    282       ASP/GLU-RICH (HIGHLY ACIDIC).
FT   DOMAIN      308    366       BPTI/KUNITZ INHIBITOR.
FT   ACT_SITE    322    323       REACTIVE BOND (BY SIMILARITY).
FT   DISULFID    312    362       BY SIMILARITY.
FT   DISULFID    321    345       BY SIMILARITY.
FT   DISULFID    337    358       BY SIMILARITY.
FT   DOMAIN      218    229       POLY-GLU.
FT   CARBOHYD    628    628       O-LINKED (GLYCOSAMINOGLYCAN) (POTENTIAL).
FT   VARSPLIC    311    365       Missing (in isoform C and isoform D).
FT                                /FTId=VSP_000020.
FT   VARSPLIC    616    627       Missing (in isoform B and isoform D).
FT                                /FTId=VSP_000021.
FT   CONFLICT    575    577       DQF -> EFV (IN REF. 2).
SQ   SEQUENCE   765 AA;  86882 MW;  CF51FCCCE305A0CF CRC64;

  Query Match             67.8%;  Score 238;  DB 1;  Length 765;
  Best Local Similarity   64.4%;  Pred. No. 1.1e-20;
  Matches   38;  Conservative   11;  Mismatches   10;  Indels    0;  Gaps    0;

Qy          3 VREVCSEQAETGPCRAAIYHWYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMAVCGSAI 61
              |: |||::| |||||| :  ||||:::|||  | ||||||||||::|:|||||| : |
Db        308 VKAVCSQEAMTGPCRAVMPRWYFDLSKGKCVRFIYGGCGGNRNNFESEDYCMAVCKTMI 366


RESULT 11
A4_FUGRU
ID   A4_FUGRU       STANDARD;      PRT;   737 AA.
AC   O93279;
DT   10-OCT-2003 (Rel. 42, Created)
DT   10-OCT-2003 (Rel. 42, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Alzheimer's disease amyloid A4 protein homolog precursor [Contains:
DE   Beta-amyloid protein (Beta-APP) (A-beta)].
GN   APP.
OS   Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC   Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC   Tetradontoidea; Tetraodontidae; Takifugu.
OX   NCBI_TaxID=31033;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98252138; PubMed=9599080;
RA   Villard L., Tassone F., Crnogorac-Jurcevic T., Clancy K., Gardiner K.;
RT   "Analysis of pufferfish homologues of the AT-rich human APP gene.";
RL   Gene 210:17-24(1998).
CC   -!- FUNCTION: Functional neuronal receptor which couples to
CC       intracellular signaling pathway through the GTP-binding protein
CC       G(O) (By similarity).
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!- SIMILARITY: Belongs to the APP family.
CC   -!- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
CC   ----------------------------------------------------------------------
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; AF090120; AAD13392.1; -.
DR   HSSP; P05067; 1HZ3.
DR   InterPro; IPR008155; A4_APP.
DR   InterPro; IPR008154; A4_extra.
DR   InterPro; IPR001255; Beta-APP.
DR   InterPro; IPR002223; Kunitz_BPTI.
DR   Pfam; PF02177; A4_EXTRA; 1.
DR   Pfam; PF03494; Beta-APP; 1.
DR   Pfam; PF00014; Kunitz_BPTI; 1.
DR   PRINTS; PR00203; AMYLOIDA4.
DR   PRINTS; PR00759; BASICPTASE.
DR   ProDom; PD000222; Kunitz_BPTI; 1.
DR   SMART; SM00006; A4_EXTRA; 1.
DR   SMART; SM00131; KU; 1.
DR   PROSITE; PS00319; A4_EXTRA; FALSE_NEG.
DR   PROSITE; PS00320; A4_INTRA; 1.
DR   PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR   PROSITE; PS50279; BPTI_KUNITZ_2; 1.
KW   Glycoprotein; Amyloid; Neurone; Transmembrane; Signal;
KW   Serine protease inhibitor.
FT   SIGNAL        1     18       POTENTIAL.
FT   CHAIN        19    737       ALZHEIMER'S DISEASE AMYLOID A4
FT                                PROTEIN HOMOLOG.
FT   CHAIN       639    681       BETA-AMYLOID PROTEIN (POTENTIAL).
FT   DOMAIN       19    668       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    669    689       POTENTIAL.
FT   DOMAIN      690    737       CYTOPLASMIC (POTENTIAL).
FT   DOMAIN      286    344       BPTI/KUNITZ INHIBITOR.
FT   SITE        726    729       CLATHRIN-BINDING (BY SIMILARITY).
FT   ACT_SITE    300    301       REACTIVE BOND.
FT   DISULFID    290    340       BY SIMILARITY.
FT   DISULFID    299    323       BY SIMILARITY.
FT   DISULFID    315    336       BY SIMILARITY.
FT   CARBOHYD    522    522       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   737 AA;  82856 MW;  6FAD01E2E3B2B7E2 CRC64;

  Query Match             67.2%;  Score 236;  DB 1;  Length 737;
  Best Local Similarity   62.3%;  Pred. No. 1.8e-20;
  Matches   38;  Conservative   11;  Mismatches   12;  Indels    0;  Gaps    0;

Qy          1 EVVREVCSEQAETGPCRAAIYHWYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMAVCGSA 60
              |||| ||  |||:|||||  :  |||:  : :| || :|||||||||::||||:||| |:
Db        284 EVVRAVCWAQAESGPCRAMLERWYFNPKKRRCVPFLFGGCGGNRNNFESEEYCLAVCSSS 343

Qy         61 I 61
              :
Db        344 L 344


RESULT 12
A4_TETFL
ID   A4_TETFL       STANDARD;      PRT;   780 AA.
AC   O73683;
DT   10-OCT-2003 (Rel. 42, Created)
DT   10-OCT-2003 (Rel. 42, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Alzheimer's disease amyloid A4 protein homolog precursor [Contains:
DE   Beta-amyloid protein (Beta-APP) (A-beta)].
GN   APP.
OS   Tetraodon fluviatilis (Puffer fish).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC   Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC   Tetradontoidea; Tetraodontidae; Tetraodon.
OX   NCBI_TaxID=47145;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98252138; PubMed=9599080;
RA   Villard L., Tassone F., Crnogorac-Jurcevic T., Clancy K., Gardiner K.;
RT   "Analysis of pufferfish homologues of the AT-rich human APP gene.";
RL   Gene 210:17-24(1998).
CC   -!- FUNCTION: Functional neuronal receptor which couples to
CC       intracellular signaling pathway through the GTP-binding protein
CC       G(O) (By similarity).
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!- SIMILARITY: Belongs to the APP family.
CC   -!- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
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CC   ---------------------------------------------------------------------
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CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AF018165; AAC41275.1; -.
DR   HSSP; P05067; 1HZ3.
DR   InterPro; IPR008155; A4_APP.
DR   InterPro; IPR008154; A4_extra.
DR   InterPro; IPR001255; Beta-APP.
DR   InterPro; IPR002223; Kunitz_BPTI.
DR   Pfam; PF02177; A4_EXTRA; 1.
DR   Pfam; PF03494; Beta-APP; 1.
DR   Pfam; PF00014; Kunitz_BPTI; 1.
DR   PRINTS; PR00203; AMYLOIDA4.
DR   PRINTS; PR00759; BASICPTASE.
DR   ProDom; PD000222; Kunitz_BPTI; 1.
DR   SMART; SM00006; A4_EXTRA; 1.
DR   SMART; SM00131; KU; 1.
DR   PROSITE; PS00319; A4_EXTRA; 1.
DR   PROSITE; PS00320; A4_INTRA; 1.
DR   PROSITE; PS00280; BPTI_KUNITZ_1; FALSE_NEG.
DR   PROSITE; PS50279; BPTI_KUNITZ_2; 1.
KW   Glycoprotein; Amyloid; Neurone; Transmembrane; Signal;
KW   Serine protease inhibitor.
FT   SIGNAL        1     18       POTENTIAL.
FT   CHAIN        19    780       ALZHEIMER'S DISEASE AMYLOID A4 PROTEIN
FT                                HOMOLOG.
FT   CHAIN       682    724       BETA-AMYLOID PROTEIN (POTENTIAL).
FT   DOMAIN       19    711       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    712    732       POTENTIAL.
FT   DOMAIN      733    780       CYTOPLASMIC (POTENTIAL).
FT   DOMAIN      323    382       BPTI/KUNITZ INHIBITOR.
FT   SITE        769    772       CLATHRIN-BINDING (BY SIMILARITY).
FT   DISULFID    327    378       BY SIMILARITY.
FT   DISULFID    336    361       BY SIMILARITY.
FT   CARBOHYD    560    560       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   780 AA;  88238 MW;  60071BE94520191D CRC64;

  Query Match             55.7%;  Score 195.5;  DB 1;  Length 780;
  Best Local Similarity   53.2%;  Pred. No. 1.2e-15;
  Matches   33;  Conservative   10;  Mismatches   18;  Indels    1;  Gaps    1;

Qy          1 EVVREVCSEQAETGPCRAAIYHWYFDVTEGKCA-PFFYGGCGGNRNNFDTEEYCMAVCGS 59
              ||||  |   |:|||| |::  |||| :|:     ||||||| |||::||||::|| |
Db        321 EVVRMFCWAHADTGPCTASMPSWYFDAVDGRTMYELMYGGCGGNMNNFESEEYCLSVCSS 380

Qy         60 AI 61
               :
Db        381 VV 382


RESULT 13
SPT2_HUMAN
ID   SPT2_HUMAN     STANDARD;      PRT;   252 AA.
AC   O43291; O00271; O14895; Q969E0;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   15-MAR-2004 (Rel. 43, Last annotation update)
DE   Kunitz-type protease inhibitor 2 precursor (Hepatocyte growth factor
DE   activator inhibitor type 2) (HAI-2) (Placental bikunin).
GN   SPINT2 OR HAI2 OR KOP.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98010584; PubMed=9346890;
RA   Kawaguchi T., Qin L., Shimomura T., Kondo J., Matsumoto K., Denda K.,
RA   Kitamura N.;
RT   "Purification and cloning of hepatocyte growth factor activator
RT   inhibitor type 2, a Kunitz-type serine protease inhibitor.";
RL   J. Biol. Chem. 272:27558-27564(1997).
RN   [2]
RP   SEQUENCE FROM N.A., AND SEQUENCE OF 28-74.
RC   TISSUE=Placenta;
RX   MEDLINE=97277372; PubMed=9115294;
RA   Marlor C.W., Delaria K.A., Davis G., Muller D.K., Greve J.M.,
RA   Tamburini P.P.;
RT   "Identification and cloning of human placental bikunin, a novel serine
RT   protease inhibitor containing two Kunitz domains.";
RL   J. Biol. Chem. 272:12202-12208(1997).
RN   [3]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Pancreatic cancer;
RX   MEDLINE=98094245; PubMed=9434156;
RA   Mueller-Pillasch F., Wallrapp C., Bartels K., Varga G., Friess H.,
RA   Buechler M., Adler G., Gress T.M.;
RT   "Cloning of a new Kunitz-type protease inhibitor with a putative
RT   transmembrane domain overexpressed in pancreatic cancer.";
RL   Biochim. Biophys. Acta 1395:88-95(1998).
RN   [4]
RP   SEQUENCE FROM N.A., AND VARIANT LEU-200.
RC   TISSUE=Colon, and Ovary;
RX   MEDLINE=22388257; PubMed=12477932;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length
RT   human and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC   -!- FUNCTION: Inhibitor of HGF activator. Also inhibits plasmin,
CC       plasma and tissue kallikrein, and factor XIa.
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein (Potential).
CC   -!- TISSUE SPECIFICITY: Expressed in placenta, kidney, pancreas,
CC       prostate, testis, thymus, and trachea.
CC   -!- DOMAIN: This inhibitor contains two inhibitory domains.
CC   -!- SIMILARITY: Contains 2 BPTI/Kunitz inhibitor domains.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AB006534; BAA25024.1; -.
DR   EMBL; U78095; AAC02781.1; -.
DR   EMBL; AF027205; AAB84031.1; -.
DR   EMBL; BC001668; AAH01668.1; -.
DR   EMBL; BC007705; AAH07705.1; -.
DR   EMBL; BC011951; AAH11951.1; -.
DR   EMBL; BC011955; AAH11955.1; -.
DR   EMBL; BC012868; AAH12868.1; -.
DR   HSSP; P05067; 1AAP.
DR   Genew; HGNC:11247; SPINT2.
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DR   MIM; 605124; -.
DR   GO; GO:0005576; C:extracellular; TAS.
DR   GO; GO:0016021; C:integral to membrane; TAS.
DR   GO; GO:0005625; C:soluble fraction; TAS.
DR   GO; GO:0004867; F:serine protease inhibitor activity; TAS.
DR   GO; GO:0006928; P:cell motility; TAS.
DR   InterPro; IPR002223; Kunitz_BPTI.
DR   Pfam; PF00014; Kunitz_BPTI; 2.
DR   PRINTS; PR00759; BASICPTASE.
DR   ProDom; PD000222; Kunitz_BPTI; 2.
DR   SMART; SM00131; KU; 2.
DR   PROSITE; PS00280; BPTI_KUNITZ_1; 2.
DR   PROSITE; PS50279; BPTI_KUNITZ_2; 2.
KW   Serine protease inhibitor; Repeat; Glycoprotein; Transmembrane;
KW   Signal; Polymorphism.
FT   SIGNAL       1     27
FT   CHAIN       28    252       KUNITZ-TYPE PROTEASE INHIBITOR 2.
FT   DOMAIN      28    197       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM   198    218       POTENTIAL.
FT   DOMAIN     219    252       CYTOPLASMIC (POTENTIAL).
FT   DOMAIN      38     88       BPTI/KUNITZ INHIBITOR 1.
FT   DOMAIN     133    183       BPTI/KUNITZ INHIBITOR 2.
FT   DISULFID    38     88       BY SIMILARITY.
FT   DISULFID    47     71       BY SIMILARITY.
FT   DISULFID    63     84       BY SIMILARITY.
FT   ACT_SITE    48     49       REACTIVE BOND (BY SIMILARITY).
FT   DISULFID   133    183       BY SIMILARITY.
FT   DISULFID   142    166       BY SIMILARITY.
FT   DISULFID   158    179       BY SIMILARITY.
FT   ACT_SITE   143    144       REACTIVE BOND (BY SIMILARITY).
FT   CARBOHYD    57     57       N-LINKED (GLCNAC. . .).
FT   CARBOHYD    94     94       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   VARIANT    200    200       V -> L.
FT                               /FTId=VAR_012482.
FT   CONFLICT     3      3       Q -> H (IN REF. 3).
FT   CONFLICT    11     11       R -> P (IN REF. 1).
FT   CONFLICT    53     53       R -> K (IN REF. 3).
FT   CONFLICT   240    240       D -> H (IN REF. 3).
SQ   SEQUENCE   252 AA;  28228 MW;  A7D3360C0EECAB2B CRC64;

  Query Match             48.1%;  Score 169;  DB 1;  Length 252;
  Best Local Similarity   52.8%;  Pred. No. 5.9e-13;
  Matches   28;  Conservative    6;  Mismatches   19;  Indels    0;  Gaps    0;

Qy          5 EVCSEQAETGPCRAAIYHWYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMAVC 57
              | |:  | ||||||:   |||||     | | |||| ||:|:: :|| ||  |
Db        131 EYCTANAVTGPCRASFPRWYFDVERNSCNNFIYGGCRGNKNSYRSEEACMLRC 183


RESULT 14
ISH1_STOHE
ID   ISH1_STOHE     STANDARD;      PRT;     55 AA.
AC   P31713;
DT   01-JUL-1993 (Rel. 26, Created)
DT   01-JUL-1993 (Rel. 26, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   Kunitz-type proteinase inhibitor SHPI-1.
OS   Stoichactis helianthus (Carribean sea anemone) (Stichodactyla
OS   helianthus).
OC   Eukaryota; Metazoa; Cnidaria; Anthozoa; Zoantharia; Actiniaria;
OC   Stichodactylidae; Stichodactyla.
OX   NCBI_TaxID=6123;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=97179757; PubMed=9027993;
RA   Delfin J., Martinez I., Antuch W., Morera V., Gonzalez Y.,
RA   Rodriguez R., Marquez M., Saroyan A., Larionova N., Diaz J.,
RA   Padron G., Chavez M.;
RT   "Purification, characterization and immobilization of proteinase
RT   inhibitors from Stichodactyla helianthus.";
RL   Toxicon 34:1367-1376(1996).
RN   [2]
RP   STRUCTURE BY NMR, AND DISULFIDE BONDS.
RX   MEDLINE=93215644; PubMed=8462542;
RA   Antuch W., Berndt K.D., Chavez M.A., Delfin J., Wuethrich K.;
RT   "The NMR solution structure of a Kunitz-type proteinase inhibitor
RT   from the sea anemone Stichodactyla helianthus.";
RL   Eur. J. Biochem. 212:675-684(1993).
CC   -!- FUNCTION: Active against serine, cysteine, and aspartic
CC       proteinases.
CC   -!- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
DR   PIR; S30332; S30332.
DR   PDB; 1SHP; 31-JAN-94.
DR   InterPro; IPR002223; Kunitz_BPTI.
DR   Pfam; PF00014; Kunitz_BPTI; 1.
DR   PRINTS; PR00759; BASICPTASE.
DR   ProDom; PD000222; Kunitz_BPTI; 1.
DR   SMART; SM00131; KU; 1.
DR   PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR   PROSITE; PS50279; BPTI_KUNITZ_2; 1.
KW   Serine protease inhibitor; 3D-structure.
FT   DISULFID     3     53
FT   DISULFID    12     36
FT   DISULFID    28     49
FT   ACT_SITE    13     14       REACTIVE BOND (TRYPSIN).
FT   HELIX        2      4
FT   STRAND      17     22
FT   TURN        23     26
FT   STRAND      27     32
FT   TURN        36     37
FT   STRAND      43     43
FT   HELIX       46     53
SQ   SEQUENCE   55 AA;  6116 MW;  532B96E3127000D4 CRC64;

  Query Match             47.9%;  Score 168;  DB 1;  Length 55;
  Best Local Similarity   51.9%;  Pred. No. 1.8e-13;
  Matches   27;  Conservative    6;  Mismatches   19;  Indels    0;  Gaps    0;

Qy          6 VCSEQAETGPCRAAIYHWYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMAVC 57
              :|||  : | |:     :|||   ||| || ||||||| |||:|   | |:|
Db          2 ICSEPKKVGRCKGYFPRFYFDSETGKCTPFIYGGCGGNGNNFETLHQCRAIC 53


RESULT 15
SPT2_MOUSE
ID   SPT2_MOUSE     STANDARD;      PRT;   252 AA.
AC   Q9WU03; Q9WU04; Q9WU05;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   Kunitz-type protease inhibitor 2 precursor (Hepatocyte growth factor
DE   activator inhibitor type 2) (HAI-2).
GN   SPINT2 OR HAI2.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
RC   STRAIN=BALB/c;
RX   MEDLINE=99160423; PubMed=10049781;
RA   Itoh H., Kataoka H., Hamasuna R., Kitamura N., Koono M.;
RT   "Hepatocyte growth factor activator inhibitor type 2 lacking the first
RT   Kunitz-type serine proteinase inhibitor domain is a predominant
RT   product in mouse but not in human.";
RL   Biochem. Biophys. Res. Commun. 255:740-748(1999).
CC   -!- FUNCTION: Inhibitor of HGF activator.
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein (Potential).
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=3;
CC       Name=1;
CC         IsoId=Q9WU03-1; Sequence=Displayed;
CC       Name=2;
CC         IsoId=Q9WU03-2; Sequence=VSP_003034;
CC       Name=3;
CC         IsoId=Q9WU03-3; Sequence=VSP_003034, VSP_003035, VSP_003036;
```

```
CC   -!- TISSUE SPECIFICITY: Isoform 2 is more predominantly expressed than
CC       isoform 1.
CC   -!- DOMAIN: This inhibitor contains two inhibitory domains.
CC   -!- SIMILARITY: Contains 2 BPTI/Kunitz inhibitor domains.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AF099016; AAD22172.1; -.
DR   EMBL; AF099019; AAD22173.1; -.
DR   EMBL; AF099020; AAD22174.1; -.
DR   HSSP; P05067; 1CA0.
DR   MGD; MGI:1338031; Spint2.
DR   InterPro; IPR002223; Kunitz_BPTI.
DR   Pfam; PF00014; Kunitz_BPTI; 2.
DR   PRINTS; PR00759; BASICPTASE.
DR   ProDom; PD000222; Kunitz_BPTI; 2.
DR   SMART; SM00131; KU; 2.
DR   PROSITE; PS00280; BPTI_KUNITZ_1; 2.
DR   PROSITE; PS50279; BPTI_KUNITZ_2; 2.
KW   Serine protease inhibitor; Repeat; Glycoprotein; Transmembrane;
KW   Signal; Alternative splicing.
FT   SIGNAL       1     27       POTENTIAL.
FT   CHAIN       28    252       KUNITZ-TYPE PROTEASE INHIBITOR 2.
FT   DOMAIN      28    197       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    198   218       POTENTIAL.
FT   DOMAIN      219   252       CYTOPLASMIC (POTENTIAL).
FT   DOMAIN       38    88       BPTI/KUNITZ INHIBITOR 1.
FT   DOMAIN      133   183       BPTI/KUNITZ INHIBITOR 2.
FT   DISULFID     38    88       BY SIMILARITY.
FT   DISULFID     47    71       BY SIMILARITY.
FT   DISULFID     63    84       BY SIMILARITY.
FT   ACT_SITE     48    49       REACTIVE BOND (BY SIMILARITY).
FT   DISULFID    133   183       BY SIMILARITY.
FT   DISULFID    142   166       BY SIMILARITY.
FT   DISULFID    158   179       BY SIMILARITY.
FT   ACT_SITE    143   144       REACTIVE BOND (BY SIMILARITY).
FT   CARBOHYD     57    57       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD     94    94       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   VARSPLIC     37    93       Missing (in isoform 2 and isoform 3).
FT                               /FTId=VSP_003034.
FT   VARSPLIC    114   128       PRKQSAEDLSAEIFN -> CFVELSVAALFLFYA (in
FT                               isoform 3).
FT                               /FTId=VSP_003035.
FT   VARSPLIC    129   252       Missing (in isoform 3).
FT                               /FTId=VSP_003036.
SQ   SEQUENCE   252 AA;  27914 MW;  B2FF4B86924D4F8F CRC64;

  Query Match           45.9%;  Score 161;  DB 1;  Length 252;
  Best Local Similarity  45.5%;  Pred. No. 5.2e-12;
  Matches   25;  Conservative   10;  Mismatches   20;  Indels    0;  Gaps    0;

Qy          3 VREVCSEQAETGPCRAAIYHWYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMAVC 57
              | | |       | |||:|  |::::|:| | || |||| || ||: ::| |:  |
Db         34 VHESCGVSKVVGKCRASIPRWWYNITDGSCQPFVYGGCEGNGNNYQSKEECLDKC 88


Search completed: April  8, 2004, 09:32:13
Job time : 12 secs
```

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: April 8, 2004, 09:30:32 ; Search time 40 Seconds
(without alignments)
481.165 Million cell updates/sec

Title: US-10-076-604-208
Perfect score: 351
Sequence: 1 EVVREVCSEQAETGPCRAAI.....GNRNNFDTEEYCMAVCGSAI 61

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_25:*
1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	319	90.9	160	11	Q9QZ78	Q9qz78 cavia sp. p
2	314	89.5	751	13	Q9DGJ7	Q9dgj7 gallus gall
3	288	82.1	747	13	Q91963	Q91963 xenopus. ap
4	238	67.8	523	4	Q14594	Q14594 homo sapien
5	238	67.8	738	13	Q90W28	Q90w28 brachydanio
6	238	67.8	751	11	Q60709	Q60709 mus musculu
7	238	67.8	763	11	Q61482	Q61482 mus musculu
8	223	63.5	82	13	Q7ZZT3	Q7zzt3 brachydanio
9	179	51.0	3198	5	Q9U8G8	Q9u8g8 manduca sex
10	168	47.9	2772	5	Q9VAV4	Q9vav4 drosophila
11	168	47.9	2776	5	Q869A0	Q869a0 drosophila
12	168	47.9	2898	5	Q868Z9	Q868z9 drosophila
13	167	47.6	137	6	Q9BDL0	Q9bdl0 oryctolagus
14	163	46.4	759	5	Q8IT91	Q8it91 ancylostoma
15	161	45.9	195	11	Q9D8Q8	Q9d8q8 mus musculu
16	161	45.9	1572	5	O44938	O44938 haemonchus
17	160	45.6	2225	5	O45881	O45881 caenorhabdi
18	158	45.0	143	4	Q86TP9	Q86tp9 homo sapien
19	158	45.0	984	5	Q9GQN2	Q9gqn2 calliactis
20	158	45.0	984	5	Q9GQN1	Q9gqn1 calliactis
21	157	44.7	142	5	Q8WPI2	Q8wpi2 boophilus m
22	157	44.7	1487	5	Q8MPV5	Q8mpv5 caenorhabdi
23	157	44.7	1558	5	Q8I7I0	Q8i7i0 caenorhabdi
24	157	44.7	2167	5	O76840	O76840 caenorhabdi
25	156	44.4	142	5	Q8WPI3	Q8wpi3 boophilus m
26	155	44.2	82	5	Q8MVB4	Q8mvb4 ixodes scap
27	153	43.6	342	13	P70004	P70004 xenopus lae
28	153	43.6	342	13	Q7SZ46	Q7sz46 xenopus lae
29	152	43.3	133	6	Q8HZ45	Q8hz45 papio papio
30	152	43.3	277	13	Q8AYE1	Q8aye1 brachydanio
31	152	43.3	279	13	Q7ZZ42	Q7zz42 brachydanio
32	151	43.0	1949	5	Q8MXG3	Q8mxg3 caenorhabdi
33	148	42.2	83	13	Q90WA0	Q90wa0 pseudonaja
34	148	42.2	83	13	Q90WA1	Q90wa1 pseudonaja
35	147	41.9	349	11	Q9DBJ9	Q9dbj9 mus musculu
36	147	41.9	349	11	Q925W1	Q925w1 mus musculu
37	146	41.6	979	4	Q8N4Z1	Q8n4z1 homo sapien
38	144	41.0	154	6	Q9N0X3	Q9n0x3 ovis aries
39	144	41.0	507	11	Q9D3K4	Q9d3k4 mus musculu
40	144	41.0	507	11	Q99J04	Q99j04 mus musculu
41	143	40.7	151	4	P78491	P78491 homo sapien
42	143	40.7	2174	5	Q9GQR0	Q9gqr0 drosophila
43	142	40.5	1743	5	Q9XWX5	Q9xwx5 caenorhabdi
44	141	40.2	132	5	Q9VQT9	Q9vqt9 drosophila
45	141	40.2	234	6	Q7YRQ8	Q7yrq8 bos taurus

ALIGNMENTS

RESULT 1
Q9QZ78
ID Q9QZ78 PRELIMINARY; PRT; 160 AA.
AC Q9QZ78;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Putative amyloid protein (Fragment).
OS Cavia sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
OX NCBI_TaxID=10143;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lens;
RA Frederikse P.H., Carper D., Farnsworth J.P., Zigler J.S.;
RT "Prion and Alzheimer precursor protein expression in a hereditary
RT guinea pig cataract.";
RL Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AF197164; AAF08934.1; -.
DR HSSP; P05067; 1AAP.
DR GO; GO:0004867; F:serine protease inhibitor activity; IEA.
DR InterPro; IPR002223; Kunitz_BPTI.
DR Pfam; PF00014; Kunitz_BPTI; 1.
DR PRINTS; PR00759; BASICPTASE.
DR ProDom; PD000222; Kunitz_BPTI; 1.
DR SMART; SM00131; KU; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS50279; BPTI_KUNITZ_2; 1.
KW Protease inhibitor; Serine protease inhibitor.
FT NON_TER 1 1
FT NON_TER 160 160
SQ SEQUENCE 160 AA; 17424 MW; 9F28C3E92E7F47C1 CRC64;

Query Match 90.9%; Score 319; DB 11; Length 160;
Best Local Similarity 90.2%; Pred. No. 8.6e-35;
Matches 55; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 1 EVVREVCSEQAETGPCRAAIYHWYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMAVCGSA 60

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                ||||||||||||||||||: |  ||||||||||||||||||||||||||||||||||||||
Db         61 EVVREVCSEQAETGPCRSMISRWYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMAVCGSV 120

Qy         61 I 61
              :
Db        121 M 121


RESULT 2
Q9DGJ7
ID   Q9DGJ7      PRELIMINARY;      PRT;   751 AA.
AC   Q9DGJ7;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Beta-amyloid precursor protein 751 isoform.
OS   Gallus gallus (Chicken).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC   Gallus.
OX   NCBI_TaxID=9031;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Sarasa M., Rodolosse A., Sorribas V.;
RT   "Cloning of full-length chicken beta-amyloid precursor protein
RT   isoforms.";
RL   Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF289219; AAG00594.1; -.
DR   HSSP; P05067; 1BA4.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0004867; F:serine protease inhibitor activity; IEA.
DR   InterPro; IPR008155; A4_APP.
DR   InterPro; IPR008154; A4_extra.
DR   InterPro; IPR001255; Beta-APP.
DR   InterPro; IPR002223; Kunitz_BPTI.
DR   Pfam; PF02177; A4_EXTRA; 1.
DR   Pfam; PF03494; Beta-APP; 1.
DR   Pfam; PF00014; Kunitz_BPTI; 1.
DR   PRINTS; PR00203; AMYLOIDA4.
DR   PRINTS; PR00759; BASICPTASE.
DR   ProDom; PD000222; Kunitz_BPTI; 1.
DR   SMART; SM00006; A4_EXTRA; 1.
DR   SMART; SM00131; KU; 1.
DR   PROSITE; PS00319; A4_EXTRA; 1.
DR   PROSITE; PS00320; A4_INTRA; 1.
DR   PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR   PROSITE; PS50279; BPTI_KUNITZ_2; 1.
KW   Protease inhibitor; Serine protease inhibitor.
SQ   SEQUENCE   751 AA;  84705 MW;  E78E9413A8033D84 CRC64;

  Query Match             89.5%;  Score 314;  DB 13;  Length 751;
  Best Local Similarity   88.5%;  Pred. No. 2.2e-33;
  Matches   54;  Conservative    2;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          1 EVVREVCSEQAETGPCRAAIYHWYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMAVCGSA 60
              |||||||||||||||||| |  ||||| ||||||||||||||||||:||||||||||
Db        285 EVVREVCSEQAETGPCRAMISRWYFDVAEGKCAPFFYGGCGGNRNNFDSEEYCMAVCGSV 344

Qy         61 I 61
              :
Db        345 L 345


RESULT 3
Q91963
ID   Q91963      PRELIMINARY;      PRT;   747 AA.
AC   Q91963;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   APP747.
GN   APP747.
OS   Xenopus.
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
OC   Xenopodinae.
OX   NCBI_TaxID=8353;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=93129227; PubMed=1282805;
RA   Okado H., Okamoto H.;
RT   "A Xenopus homologue of the human beta-amyloid precursor protein:
RT   developmental regulation of its gene expression.";
RL   Biochem. Biophys. Res. Commun. 189:1561-1568(1992).
DR   EMBL; S52417; AAB24853.1; -.
DR   HSSP; P05067; 1HZ3.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0004867; F:serine protease inhibitor activity; IEA.
DR   InterPro; IPR008155; A4_APP.
DR   InterPro; IPR008154; A4_extra.
DR   InterPro; IPR001255; Beta-APP.
DR   InterPro; IPR002223; Kunitz_BPTI.
DR   Pfam; PF02177; A4_EXTRA; 1.
DR   Pfam; PF03494; Beta-APP; 1.
DR   Pfam; PF00014; Kunitz_BPTI; 1.
DR   PRINTS; PR00203; AMYLOIDA4.
DR   PRINTS; PR00759; BASICPTASE.
DR   ProDom; PD000222; Kunitz_BPTI; 1.
DR   SMART; SM00131; KU; 1.
DR   PROSITE; PS00319; A4_EXTRA; 1.
DR   PROSITE; PS00320; A4_INTRA; 1.
DR   PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR   PROSITE; PS50279; BPTI_KUNITZ_2; 1.
KW   Protease inhibitor; Serine protease inhibitor.
SQ   SEQUENCE   747 AA;  84893 MW;  A75E81885681D948 CRC64;

  Query Match             82.1%;  Score 288;  DB 13;  Length 747;
  Best Local Similarity   80.3%;  Pred. No. 6.6e-30;
  Matches   49;  Conservative    5;  Mismatches    7;  Indels    0;  Gaps    0;

Qy          1 EVVREVCSEQAETGPCRAAIYHWYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMAVCGSA 60
              |||||||||||||||||| |  ||:|||| ||| | ||||||||||:::|||||||||
Db        281 EVVREVCSEQAETGPCRAMISRWYYDVTESKCAQFIYGGCGGNRNNFESDDYCMAVCGSV 340

Qy         61 I 61
              |
Db        341 I 341


RESULT 4
Q14594
ID   Q14594      PRELIMINARY;      PRT;   523 AA.
AC   Q14594;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Binding protein (Fragment).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RA   Vostrov A.A., Quitschke W.W., Schwarzman A.L., Blangy A., Cuzin F.,
RA   Wesley U.V., Hagag N.G., Goldgaber D.;
RT   "Cloning of a protein that binds to a recognition sequence in the APP
RT   promoter.";
RL   Submitted (AUG-1993) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; L23113; AAA36032.1; -.
DR   HSSP; P05067; 1CA0.
DR   GO; GO:0004867; F:serine protease inhibitor activity; IEA.
DR   InterPro; IPR008155; A4_APP.
DR   InterPro; IPR002223; Kunitz_BPTI.
DR   Pfam; PF00014; Kunitz_BPTI; 1.
DR   PRINTS; PR00203; AMYLOIDA4.
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DR   PRINTS; PR00759; BASICPTASE.
DR   ProDom; PD000222; Kunitz_BPTI; 1.
DR   SMART; SM00131; KU; 1.
DR   PROSITE; PS00320; A4_INTRA; 1.
DR   PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR   PROSITE; PS50279; BPTI_KUNITZ_2; 1.
KW   Protease inhibitor; Serine protease inhibitor.
FT   NON_TER       1      1
SQ   SEQUENCE   523 AA;  60035 MW;  5E6FC830DFEA551C CRC64;

  Query Match             67.8%;  Score 238;  DB 4;  Length 523;
  Best Local Similarity   64.4%;  Pred. No. 2.3e-23;
  Matches   38;  Conservative   11;  Mismatches   10;  Indels    0;  Gaps    0;

Qy          3 VREVCSEQAETGPCRAAIYHWYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMAVCGSAI 61
              |: |||::| |||||| :  ||||:::|||  | ||||||||||::|:|||||| : |
Db         78 VKAVCSQEAMTGPCRAVMPRWYFDLSKGKCVRFIYGGCGGNRNNFESEDYCMAVCKAMI 136


RESULT 5
Q90W28
ID   Q90W28      PRELIMINARY;      PRT;   738 AA.
AC   Q90W28;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Amyloid precursor protein.
GN   APPA OR APP.
OS   Brachydanio rerio (Zebrafish) (Danio rerio).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC   Cyprinidae; Danio.
OX   NCBI_TaxID=7955;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Groth C., Lardelli M.;
RT   "Expression analysis of zebrafish app.";
RL   Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF389401; AAK64495.1; -.
DR   ZFIN; ZDB-GENE-000616-13; appa.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0004867; F:serine protease inhibitor activity; IEA.
DR   InterPro; IPR008155; A4_APP.
DR   InterPro; IPR008154; A4_extra.
DR   InterPro; IPR001255; Beta-APP.
DR   InterPro; IPR002223; Kunitz_BPTI.
DR   Pfam; PF02177; A4_EXTRA; 1.
DR   Pfam; PF03494; Beta-APP; 1.
DR   Pfam; PF00014; Kunitz_BPTI; 1.
DR   PRINTS; PR00203; AMYLOIDA4.
DR   PRINTS; PR00759; BASICPTASE.
DR   ProDom; PD000222; Kunitz_BPTI; 1.
DR   SMART; SM00006; A4_EXTRA; 1.
DR   SMART; SM00131; KU; 1.
DR   PROSITE; PS00319; A4_EXTRA; 1.
DR   PROSITE; PS00320; A4_INTRA; 1.
DR   PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR   PROSITE; PS50279; BPTI_KUNITZ_2; 1.
KW   Protease inhibitor; Serine protease inhibitor.
SQ   SEQUENCE   738 AA;  83577 MW;  AF480F6D308FD298 CRC64;

  Query Match             67.8%;  Score 238;  DB 13;  Length 738;
  Best Local Similarity   63.9%;  Pred. No. 3.4e-23;
  Matches   39;  Conservative    8;  Mismatches   14;  Indels    0;  Gaps    0;

Qy          1 EVVREVCSEQAETGPCRAAIYHWYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMAVCGSA 60
              |||||||   ||||||||  :  ||:   | :|||| ||||||||||||::|||||::||
Db        287 EVVREVCFASAETGPCRAMLSRWYYVREERRCAPFIYGGCGGNRNNFESEEYCLSVCSGV 346

Qy         61 I 61
              :
Db        347 L 347
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RESULT 6
Q60709
ID   Q60709      PRELIMINARY;      PRT;   751 AA.
AC   Q60709;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Amyloid precursor-like protein 2, isoform 751.
GN   APLP2.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=ICR;
RA   Slunt H.H., Von Koch C., Sisodia S.S.;
RT   "Mouse Amyloid Precursor-Like Protein 2 (APLP2) mRNA, isoform APLP2-
RT   751,complete cds.";
RL   Submitted (OCT-1994) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE OF 1-229 FROM N.A.
RC   STRAIN=ICR;
RX   MEDLINE=94132029; PubMed=8300594;
RA   Slunt H.H., Thinakaran G., Von Koch C., Lo A.C., Tanzi R.E.,
RA   Sisodia S.S.;
RT   "Expression of a ubiquitous, cross-reactive homologue of the mouse
RT   beta-amyloid precursor protein (APP).";
RL   J. Biol. Chem. 269:2637-2644(1994).
RN   [3]
RP   SEQUENCE FROM N.A.
RC   STRAIN=ICR;
RX   MEDLINE=94350957; PubMed=8071334;
RA   Thinakaran G., Sisodia S.S.;
RT   "Amyloid precursor-like protein 2 (APLP2) is modified by the addition
RT   of chondroitin sulfate glycosaminoglycan at a single site.";
RL   J. Biol. Chem. 269:22099-22104(1994).
RN   [4]
RP   SEQUENCE FROM N.A.
RC   STRAIN=ICR;
RA   Thinakaran G.;
RL   Submitted (OCT-1994) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; U15571; AAA50603.1; -.
DR   PIR; A49974; A49974.
DR   HSSP; P05067; 1MWP.
DR   MGD; MGI:88047; Aplp2.
DR   GO; GO:0004867; F:serine protease inhibitor activity; IEA.
DR   InterPro; IPR008155; A4_APP.
DR   InterPro; IPR008154; A4_extra.
DR   InterPro; IPR002223; Kunitz_BPTI.
DR   Pfam; PF02177; A4_EXTRA; 1.
DR   Pfam; PF00014; Kunitz_BPTI; 1.
DR   PRINTS; PR00203; AMYLOIDA4.
DR   PRINTS; PR00759; BASICPTASE.
DR   ProDom; PD000222; Kunitz_BPTI; 1.
DR   SMART; SM00006; A4_EXTRA; 1.
DR   SMART; SM00131; KU; 1.
DR   PROSITE; PS00319; A4_EXTRA; 1.
DR   PROSITE; PS00320; A4_INTRA; 1.
DR   PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR   PROSITE; PS50279; BPTI_KUNITZ_2; 1.
KW   Protease inhibitor; Serine protease inhibitor.
SQ   SEQUENCE   751 AA;  85247 MW;  D183F6A4AD17BC04 CRC64;

  Query Match             67.8%;  Score 238;  DB 11;  Length 751;
  Best Local Similarity   64.4%;  Pred. No. 3.5e-23;
  Matches   38;  Conservative   11;  Mismatches   10;  Indels    0;  Gaps    0;

Qy          3 VREVCSEQAETGPCRAAIYHWYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMAVCGSAI 61
              |: |||::| |||||| :  ||||:::|||  | ||||||||||::|:|||||| : |
Db        306 VKAVCSQEAMTGPCRAVMPRWYFDLSKGKCVRFIYGGCGGNRNNFESEDYCMAVCKAMI 364
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RESULT 7
Q61482
ID   Q61482      PRELIMINARY;      PRT;   763 AA.
AC   Q61482;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   CDE1-binding protein CDEBP.
GN   CDEBP.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=B6;
RX   MEDLINE=96299736; PubMed=8661100;
RA   Yang Y., Martin L., Cuzin F., Mattei M.G., Rassoulzadegan M.;
RT   "Genomic structure and chromosomal localization of the mouse CDE1-
RT   binding protein CDEBP (APLP2) gene and promoter sequences.";
RL   Genomics 35:24-29(1996).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=B6;
RA   Luc M., Yang Y.;
RL   Submitted (OCT-1995) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; U37485; AAB38114.1; -.
DR   EMBL; U37468; AAB38114.1; JOINED.
DR   EMBL; U37469; AAB38114.1; JOINED.
DR   EMBL; U37470; AAB38114.1; JOINED.
DR   EMBL; U37471; AAB38114.1; JOINED.
DR   EMBL; U37472; AAB38114.1; JOINED.
DR   EMBL; U37473; AAB38114.1; JOINED.
DR   EMBL; U37474; AAB38114.1; JOINED.
DR   EMBL; U37475; AAB38114.1; JOINED.
DR   EMBL; U37476; AAB38114.1; JOINED.
DR   EMBL; U37477; AAB38114.1; JOINED.
DR   EMBL; U37478; AAB38114.1; JOINED.
DR   EMBL; U37479; AAB38114.1; JOINED.
DR   EMBL; U37480; AAB38114.1; JOINED.
DR   EMBL; U37481; AAB38114.1; JOINED.
DR   EMBL; U37482; AAB38114.1; JOINED.
DR   EMBL; U37483; AAB38114.1; JOINED.
DR   EMBL; U37484; AAB38114.1; JOINED.
DR   HSSP; P05067; 1MWP.
DR   GO; GO:0004867; F:serine protease inhibitor activity; IEA.
DR   InterPro; IPR008155; A4_APP.
DR   InterPro; IPR008154; A4_extra.
DR   InterPro; IPR002223; Kunitz_BPTI.
DR   Pfam; PF02177; A4_EXTRA; 1.
DR   Pfam; PF00014; Kunitz_BPTI; 1.
DR   PRINTS; PR00203; AMYLOIDA4.
DR   PRINTS; PR00759; BASICPTASE.
DR   ProDom; PD000222; Kunitz_BPTI; 1.
DR   SMART; SM00006; A4_EXTRA; 1.
DR   SMART; SM00131; KU; 1.
DR   PROSITE; PS00319; A4_EXTRA; 1.
DR   PROSITE; PS00320; A4_INTRA; 1.
DR   PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR   PROSITE; PS50279; BPTI_KUNITZ_2; 1.
KW   Protease inhibitor; Serine protease inhibitor.
SQ   SEQUENCE   763 AA;  86716 MW;  2CDC7780180619A6 CRC64;

  Query Match           67.8%;  Score 238;  DB 11;  Length 763;
  Best Local Similarity   64.4%;  Pred. No. 3.5e-23;
  Matches   38;  Conservative   11;  Mismatches   10;  Indels    0;  Gaps    0;

Qy          3 VREVCSEQAETGPCRAAIYHWYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMAVCGSAI 61
              |: |||::| |||||| :  ||||:::|||   | ||||||||||::|:|||||| : |
Db        306 VKAVCSQEAMTGPCRAVMPRWYFDLSKGKCVRFIYGGCGGNRNNFESEDYCMAVCKAMI 364

RESULT 8
Q7ZZT3
ID   Q7ZZT3      PRELIMINARY;      PRT;    82 AA.
AC   Q7ZZT3;
DT   01-JUN-2003 (TrEMBLrel. 24, Created)
DT   01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Amyloid protein b (Fragment).
GN   APPB.
OS   Brachydanio rerio (Zebrafish) (Danio rerio).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC   Cyprinidae; Danio.
OX   NCBI_TaxID=7955;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Groth C., Lardelli M.;
RT   "Kunitz-type protease inhibitor domain of zebrafish appb.";
RL   Submitted (APR-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY271744; AAP22956.1; -.
DR   GO; GO:0004867; F:serine protease inhibitor activity; IEA.
DR   InterPro; IPR002223; Kunitz_BPTI.
DR   Pfam; PF00014; Kunitz_BPTI; 1.
DR   PRINTS; PR00759; BASICPTASE.
DR   ProDom; PD000222; Kunitz_BPTI; 1.
DR   SMART; SM00131; KU; 1.
DR   PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR   PROSITE; PS50279; BPTI_KUNITZ_2; 1.
FT   NON_TER       1      1
FT   NON_TER      82     82
SQ   SEQUENCE   82 AA;  8874 MW;  0723D4AC6585B349 CRC64;

  Query Match           63.5%;  Score 223;  DB 13;  Length 82;
  Best Local Similarity   60.7%;  Pred. No. 3.2e-22;
  Matches   37;  Conservative    9;  Mismatches   15;  Indels    0;  Gaps    0;

Qy          1 EVVREVCSEQAETGPCRAAIYHWYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMAVCGSA 60
              |||| ||    | :||| | :  |||   :|:|| | :||||||||||::|||||||| |:
Db         16 EVVRAVCWAPARSGPCHAKLPRWYFVAEKGRCASFTFGGCGGNRNNFESEEYCMAVCSSS 75

Qy         61 I 61
              :
Db         76 V 76


RESULT 9
Q9U8G8
ID   Q9U8G8      PRELIMINARY;      PRT;  3198 AA.
AC   Q9U8G8;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Lacunin precursor.
OS   Manduca sexta (Tobacco hawkmoth) (Tobacco hornworm).
OC   Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC   Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Sphingiodea;
OC   Sphingidae; Sphinginae; Manduca.
OX   NCBI_TaxID=7130;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=99457716; PubMed=10528409;
RA   Nardi J.B., Martos R., Walden K.K., Lampe D.J., Robertson H.M.;
RT   "Expression of lacunin, a large multidomain extracellular matrix
RT   protein, accompanies morphogenesis of epithelial monolayers in Manduca
RT   sexta.";
RL   Insect Biochem. Mol. Biol. 29:883-897(1999).
DR   EMBL; AF078161; AAF04457.1; -.
DR   HSSP; P12111; 2KNT.
DR   GO; GO:0004867; F:serine protease inhibitor activity; IEA.
DR   InterPro; IPR004094; Antistasin.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003598; Ig_c2.
DR   InterPro; IPR002223; Kunitz_BPTI.
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DR   InterPro; IPR000884; TSP1.
DR   InterPro; IPR008197; WAP.
DR   Pfam; PF02822; Antistasin; 4.
DR   Pfam; PF00047; ig; 2.
DR   Pfam; PF00014; Kunitz_BPTI; 10.
DR   Pfam; PF00090; tsp_1; 5.
DR   Pfam; PF00095; wap; 1.
DR   PRINTS; PR00759; BASICPTASE.
DR   ProDom; PD000222; Kunitz_BPTI; 10.
DR   SMART; SM00408; IGc2; 2.
DR   SMART; SM00131; KU; 10.
DR   SMART; SM00209; TSP1; 7.
DR   SMART; SM00217; WAP; 1.
DR   PROSITE; PS00317; 4_DISULFIDE_CORE; 1.
DR   PROSITE; PS00280; BPTI_KUNITZ_1; 8.
DR   PROSITE; PS50279; BPTI_KUNITZ_2; 10.
DR   PROSITE; PS50835; IG_LIKE; 2.
DR   PROSITE; PS50092; TSP1; 5.
KW   Immunoglobulin domain; Protease inhibitor; Serine protease inhibitor;
KW   Signal.
FT   SIGNAL        1     21       POTENTIAL.
SQ   SEQUENCE   3198 AA;  349364 MW;  AB4ACD459C0D9134 CRC64;

  Query Match             51.0%;  Score 179;  DB 5;  Length 3198;
  Best Local Similarity   53.6%;  Pred. No. 1.4e-14;
  Matches   30;  Conservative    5;  Mismatches   21;  Indels    0;  Gaps    0;

Qy          5 EVCSEQAETGPCRAAIYHWYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMAVCGSA 60
              |:|  : : |||       | :|   |||  | |||||||||||| |||||   ||:|
Db       2204 EMCFMEKDPGPCTDTETRWVYDYKLGKCVTFEYGGCGGNRNNFPTEEYCQYYCGTA 2259


RESULT 10
Q9VAV4
ID   Q9VAV4      PRELIMINARY;      PRT;  2772 AA.
AC   Q9VAV4; Q9VAV3;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   CG33103-PB.
GN   PPN.
OS   Drosophila melanogaster (Fruit fly).
OC   Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC   Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC   Ephydroidea; Drosophilidae; Drosophila.
OX   NCBI_TaxID=7227;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=20196006; PubMed=10731132;
RA   Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA   Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA   George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA   Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA   Brandon R.C., Rogers Y.H., Blazej R.G., Champe M., Pfeiffer B.D.,
RA   Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L.,
RA   Abril J.F., Agbayani A., An H.J., Andrews-Pfannkoch C., Baldwin D.,
RA   Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA   Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA   Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA   Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA   Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA   de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA   Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA   Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA   Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA   Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA   Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA   Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibegwam C.,
RA   Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA   Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA   Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA   Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA   Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA   Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA   Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA   Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA   Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H.,
RA   Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA   Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA   Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA   Wang Z.Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA   Williams S.M., WoodageT, Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,
RA   Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA   Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA   Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT   "The genome sequence of Drosophila melanogaster.";
RL   Science 287:2185-2195(2000).
RN   [2]
RP   SEQUENCE FROM N.A.
RA   Celniker S.E., Adams M.D., Kronmiller B., Wan K.H., Holt R.A.,
RA   Evans C.A., Gocayne J.D., Amanatides P.G., Brandon R.C., Rogers Y.,
RA   Banzon J., An H., Baldwin D., Banzon J., Beeson K.Y., Busam D.A.,
RA   Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M.,
RA   Dodson K., Dorsett V., Doup L.E., Doyle C., Dresnek D., Farfan D.,
RA   Ferriera S., Frise E., Galle R.F., Garg N.S., George R.A.,
RA   Gonzalez M., Houck J., Hoskins R.A., Hostin D., Howland T.J.,
RA   Ibegwam C., Jalali M., Kruse D., Li P., Mattei B., Moshrefi A.,
RA   McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunoo J.,
RA   Pacleb J., Paragas V., Park S., Patel S., Pfeiffer B.,
RA   Phouanenavong S., Pittman G.S., Puri V., Richards S., Scheeler F.,
RA   Stapleton M., Strong R., Svirskas R., Tector C., Tyler D.,
RA   Williams S.M., Zaveri J.S., Smith H.O., Venter J.C., Rubin G.M.;
RT   "Sequencing of Drosophila melanogaster genome.";
RL   Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   SEQUENCE FROM N.A.
RA   Misra S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K.,
RA   Hradecky P., Huang Y., Kaminker J.S., Prochnik S.E., Smith C.D.,
RA   Tupy J.L., Bergman C.M., Berman B.P., Carlson J.W., Celniker S.E.,
RA   Clamp M.E., Drysdale R.A., Emmert D., Frise E., de Grey A.D.N.J.,
RA   Harris N.L., Kronmiller B., Marshall B., Millburn G.H., Richter J.,
RA   Russo S., Searle S.M.J., Smith E., Shu S., Smutniak F.,
RA   Whitfield E.J., Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.J.,
RA   Lewis S.E.;
RT   "Annotation of Drosophila melanogaster genome.";
RL   Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
RN   [4]
RP   SEQUENCE FROM N.A.
RA   FlyBase;
RL   Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases.
RN   [5]
RP   SEQUENCE FROM N.A.
RA   FlyBase;
RL   Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AE003765; AAF56794.3; -.
DR   GO; GO:0005604; C:basement membrane; IDA.
DR   InterPro; IPR006209; EGF_like.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003598; Ig_c2.
DR   InterPro; IPR002223; Kunitz_BPTI.
DR   InterPro; IPR000884; TSP1.
DR   InterPro; IPR008197; WAP.
DR   Pfam; PF00047; ig; 3.
DR   Pfam; PF00014; Kunitz_BPTI; 12.
DR   Pfam; PF00090; tsp_1; 5.
DR   Pfam; PF00095; wap; 1.
DR   PRINTS; PR00759; BASICPTASE.
DR   ProDom; PD000222; Kunitz_BPTI; 10.
DR   SMART; SM00409; IG; 3.
DR   SMART; SM00408; IGc2; 3.
DR   SMART; SM00131; KU; 10.
DR   SMART; SM00209; TSP1; 7.
DR   SMART; SM00217; WAP; 1.
DR   PROSITE; PS00317; 4_DISULFIDE_CORE; 1.
DR   PROSITE; PS00280; BPTI_KUNITZ_1; 9.
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DR   PROSITE; PS50279; BPTI_KUNITZ_2; 10.
DR   PROSITE; PS00022; EGF_1; 1.
DR   PROSITE; PS50835; IG_LIKE; 3.
DR   PROSITE; PS50092; TSP1; 5.
SQ   SEQUENCE   2772 AA;  299154 MW;  3965DC92D30CCAAA CRC64;

  Query Match             47.9%;  Score 168;  DB 5;  Length 2772;
  Best Local Similarity   45.6%;  Pred. No. 3.6e-13;
  Matches   26;  Conservative    9;  Mismatches   22;  Indels    0;  Gaps    0;

Qy          1 EVVREVCSEQAETGPCRAAIYHWYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMAVC 57
              :| :::|.  || | |   :  ||:|  :  |  |:|||||| | | ||| |:| |
Db       1843 QVAKDICEIPAEVGECANYVTSWYYDTQDQACRQFYYGGCGGNENRFPTEESCLARC 1899


RESULT 11
Q869A0
ID   Q869A0      PRELIMINARY;      PRT;  2776 AA.
AC   Q869A0;
DT   01-JUN-2003 (TrEMBLrel. 24, Created)
DT   01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Extracellular matrix protein papilin 2.
OS   Drosophila melanogaster (Fruit fly).
OC   Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC   Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC   Ephydroidea; Drosophilidae; Drosophila.
OX   NCBI_TaxID=7227;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=22552133; PubMed=12666201;
RA   Kramerova I.A., Kramerov A.A., Fessler J.H.;
RT   "Alternative splicing of papilin and the diversity of Drosophila
RT   extracellular matrix during embryonic morphogenesis.";
RL   Dev. Dyn. 226:634-642(2003).
DR   EMBL; AF529179; AAO84907.1; -.
DR   GO; GO:0004867; F:serine protease inhibitor activity; IEA.
DR   GO; GO:0005198; F:structural molecule activity; IEA.
DR   InterPro; IPR006209; EGF_like.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003598; Ig_c2.
DR   InterPro; IPR002223; Kunitz_BPTI.
DR   InterPro; IPR000884; TSP1.
DR   InterPro; IPR008197; WAP.
DR   Pfam; PF00047; ig; 3.
DR   Pfam; PF00014; Kunitz_BPTI; 10.
DR   Pfam; PF00090; tsp_1; 5.
DR   Pfam; PF00095; wap; 1.
DR   PRINTS; PR00759; BASICPTASE.
DR   ProDom; PD000222; Kunitz_BPTI; 10.
DR   SMART; SM00409; IG; 3.
DR   SMART; SM00408; IGc2; 3.
DR   SMART; SM00131; KU; 10.
DR   SMART; SM00209; TSP1; 7.
DR   SMART; SM00217; WAP; 1.
DR   PROSITE; PS00317; 4_DISULFIDE_CORE; 1.
DR   PROSITE; PS00280; BPTI_KUNITZ_1; 9.
DR   PROSITE; PS50279; BPTI_KUNITZ_2; 10.
DR   PROSITE; PS00022; EGF_1; 1.
DR   PROSITE; PS50835; IG_LIKE; 3.
DR   PROSITE; PS50092; TSP1; 5.
KW   Matrix protein.
SQ   SEQUENCE   2776 AA;  299741 MW;  92D38A17360D2D42 CRC64;

  Query Match             47.9%;  Score 168;  DB 5;  Length 2776;
  Best Local Similarity   45.6%;  Pred. No. 3.6e-13;
  Matches   26;  Conservative    9;  Mismatches   22;  Indels    0;  Gaps    0;

Qy          1 EVVREVCSEQAETGPCRAAIYHWYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMAVC 57
              :| :::|   || | |   :  ||:|  :  |  |:|||||| | | ||| |:| |
Db       1843 QVAKDICEIPAEVGECANYVTSWYYDTQDQACRQFYYGGCGGNENRFPTEESCLARC 1899


RESULT 12
Q868Z9
ID   Q868Z9      PRELIMINARY;      PRT;  2898 AA.
AC   Q868Z9;
DT   01-JUN-2003 (TrEMBLrel. 24, Created)
DT   01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Extracellular matrix protein papilin 3.
OS   Drosophila melanogaster (Fruit fly).
OC   Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC   Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC   Ephydroidea; Drosophilidae; Drosophila.
OX   NCBI_TaxID=7227;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=22552133; PubMed=12666201;
RA   Kramerova I.A., Kramerov A.A., Fessler J.H.;
RT   "Alternative splicing of papilin and the diversity of Drosophila
RT   extracellular matrix during embryonic morphogenesis.";
RL   Dev. Dyn. 226:634-642(2003).
DR   EMBL; AF529180; AAO84908.1; -.
DR   GO; GO:0004867; F:serine protease inhibitor activity; IEA.
DR   GO; GO:0005198; F:structural molecule activity; IEA.
DR   InterPro; IPR006209; EGF_like.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003598; Ig_c2.
DR   InterPro; IPR002223; Kunitz_BPTI.
DR   InterPro; IPR000884; TSP1.
DR   InterPro; IPR008197; WAP.
DR   Pfam; PF00047; ig; 3.
DR   Pfam; PF00014; Kunitz_BPTI; 12.
DR   Pfam; PF00090; tsp_1; 5.
DR   Pfam; PF00095; wap; 1.
DR   PRINTS; PR00759; BASICPTASE.
DR   ProDom; PD000222; Kunitz_BPTI; 12.
DR   SMART; SM00409; IG; 3.
DR   SMART; SM00408; IGc2; 3.
DR   SMART; SM00131; KU; 12.
DR   SMART; SM00209; TSP1; 7.
DR   SMART; SM00217; WAP; 1.
DR   PROSITE; PS00317; 4_DISULFIDE_CORE; 1.
DR   PROSITE; PS00280; BPTI_KUNITZ_1; 11.
DR   PROSITE; PS50279; BPTI_KUNITZ_2; 12.
DR   PROSITE; PS00022; EGF_1; 1.
DR   PROSITE; PS50835; IG_LIKE; 3.
DR   PROSITE; PS50092; TSP1; 5.
KW   Matrix protein.
SQ   SEQUENCE   2898 AA;  313250 MW;  2F992742F2D64A00 CRC64;

  Query Match             47.9%;  Score 168;  DB 5;  Length 2898;
  Best Local Similarity   45.6%;  Pred. No. 3.8e-13;
  Matches   26;  Conservative    9;  Mismatches   22;  Indels    0;  Gaps    0;

Qy          1 EVVREVCSEQAETGPCRAAIYHWYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMAVC 57
              :| :::|   || | |   :  ||:|  :  |  |:|||||| | | ||| |:| |
Db       1843 QVAKDICEIPAEVGECANYVTSWYYDTQDQACRQFYYGGCGGNENRFPTEESCLARC 1899


RESULT 13
Q9BDL0
ID   Q9BDL0      PRELIMINARY;      PRT;   137 AA.
AC   Q9BDL0;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Eppin.
OS   Oryctolagus cuniculus (Rabbit).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX   NCBI_TaxID=9986;
RN   [1]
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RP   SEQUENCE FROM N.A.
RC   TISSUE=Testis;
RA   Sivashanmugam P., Hall S.H., Hamil K.G., French F.S., O'Rand M.G.,
RA   Richardson R.T.;
RT   "Characterization of monkey and mouse Eppin, a protease inhibitor from
RT   epididymis and testis.";
RL   Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF346415; AAK31337.1; -.
DR   HSSP; P05067; 1CA0.
DR   GO; GO:0004867; F:serine protease inhibitor activity; IEA.
DR   InterPro; IPR002223; Kunitz_BPTI.
DR   InterPro; IPR008197; WAP.
DR   Pfam; PF00014; Kunitz_BPTI; 1.
DR   Pfam; PF00095; wap; 1.
DR   PRINTS; PR00759; BASICPTASE.
DR   ProDom; PD000222; Kunitz_BPTI; 1.
DR   SMART; SM00131; KU; 1.
DR   SMART; SM00217; WAP; 1.
DR   PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR   PROSITE; PS50279; BPTI_KUNITZ_2; 1.
KW   Protease inhibitor; Serine protease inhibitor.
SQ   SEQUENCE   137 AA;  15773 MW;  F397AF4E065D626B CRC64;

  Query Match             47.6%;  Score 167;  DB 6;  Length 137;
  Best Local Similarity   50.0%;  Pred. No. 1.9e-14;
  Matches   27;  Conservative    6;  Mismatches   21;  Indels    0;  Gaps    0;

Qy          4 REVCSEQAETGPCRAAIYHWYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMAVC 57
              ::|||   ||||| | |  |::|      |  | |||| || ||| ||  |: :|
Db         74 KDVCSMPKETGPCLAFIPRWWYDKEREICTEFIYGGCNGNNNNFQTEAICLVIC 127


RESULT 14
Q8IT91
ID   Q8IT91      PRELIMINARY;      PRT;   759 AA.
AC   Q8IT91;
DT   01-MAR-2003 (TrEMBLrel. 23, Created)
DT   01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Kunitz-like protease inhibitor precursor.
OS   Ancylostoma caninum (Dog hookworm).
OC   Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Strongylida;
OC   Ancylostomatoidea; Ancylostomatidae; Ancylostomatinae; Ancylostoma.
OX   NCBI_TaxID=29170;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Baltimore;
RA   Hawdon J.M., Datu B., Crowell M.;
RT   "Molecular Cloning of a Novel Multi-domain Kunitz-type Proteinase
RT   Inhibitor from the Hookworm Ancylostoma caninum.";
RL   Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF533590; AAN10061.1; -.
DR   GO; GO:0008233; F:peptidase activity; IEA.
DR   GO; GO:0004867; F:serine protease inhibitor activity; IEA.
DR   InterPro; IPR002223; Kunitz_BPTI.
DR   Pfam; PF00014; Kunitz_BPTI; 12.
DR   PRINTS; PR00759; BASICPTASE.
DR   ProDom; PD000222; Kunitz_BPTI; 10.
DR   SMART; SM00131; KU; 12.
DR   PROSITE; PS00280; BPTI_KUNITZ_1; 10.
DR   PROSITE; PS50279; BPTI_KUNITZ_2; 12.
KW   Signal; Protease.
FT   SIGNAL       1      16       POTENTIAL.
SQ   SEQUENCE   759 AA;  84886 MW;  C431A3C3F418F40A CRC64;

  Query Match             46.4%;  Score 163;  DB 5;  Length 759;
  Best Local Similarity   47.4%;  Pred. No. 4.1e-13;
  Matches   27;  Conservative    9;  Mismatches   21;  Indels    0;  Gaps    0;

Qy          1 EVVREVCSEQAETGPCRAAIYHWYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMAVC 57
              |  :| ||:  | |||:| :  : :|  : ||  |||||| ||:|||:| | |   |
Db        513 EPEKETCSQPIEAGPCKAMVRRFAYDNAKEKCVEPFYGGCKGNKNNFETMEDCTFTC 569


RESULT 15
Q9D8Q8
ID   Q9D8Q8      PRELIMINARY;      PRT;   195 AA.
AC   Q9D8Q8;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Serine protease inhibitor, kunitz type 2.
GN   SPINT2.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Pancreas;
RX   MEDLINE=21085660; PubMed=11217851;
RA   Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA   Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA   Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA   Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA   Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA   Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA   Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA   Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA   Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA   Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA   Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA   Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA   Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA   Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA   Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA   Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA   Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA   Hayashizaki Y.;
RT   "Functional annotation of a full-length mouse cDNA collection.";
RL   Nature 409:685-690(2001).
DR   EMBL; AK007792; BAB25258.1; -.
DR   HSSP; P05067; 1AAP.
DR   MGD; MGI:1338031; Spint2.
DR   GO; GO:0004867; F:serine protease inhibitor activity; IEA.
DR   InterPro; IPR002223; Kunitz_BPTI.
DR   Pfam; PF00014; Kunitz_BPTI; 1.
DR   PRINTS; PR00759; BASICPTASE.
DR   ProDom; PD000222; Kunitz_BPTI; 1.
DR   SMART; SM00131; KU; 1.
DR   PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR   PROSITE; PS50279; BPTI_KUNITZ_2; 1.
KW   Protease inhibitor; Serine protease inhibitor.
SQ   SEQUENCE   195 AA;  21705 MW;  1ABD78CEF1175DE1 CRC64;

  Query Match             45.9%;  Score 161;  DB 11;  Length 195;
  Best Local Similarity   49.1%;  Pred. No. 1.8e-13;
  Matches   26;  Conservative    8;  Mismatches   19;  Indels    0;  Gaps    0;

Qy          5 EVCSEQAETGPCRAAIYHWYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMAVC 57
              | |  :| |||||||   ||:|  :  |  | |||| ||:|:: ::| ||  |
Db         74 EYCVPKAVTGPCRAAFPRWYYDTEKNSCISFIYGGCRGNKNSYLSQEACMQHC 126


Search completed: April  8, 2004, 09:34:13
Job time : 42 secs
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